

1 2 3 4 5
a b a b a b a b a b

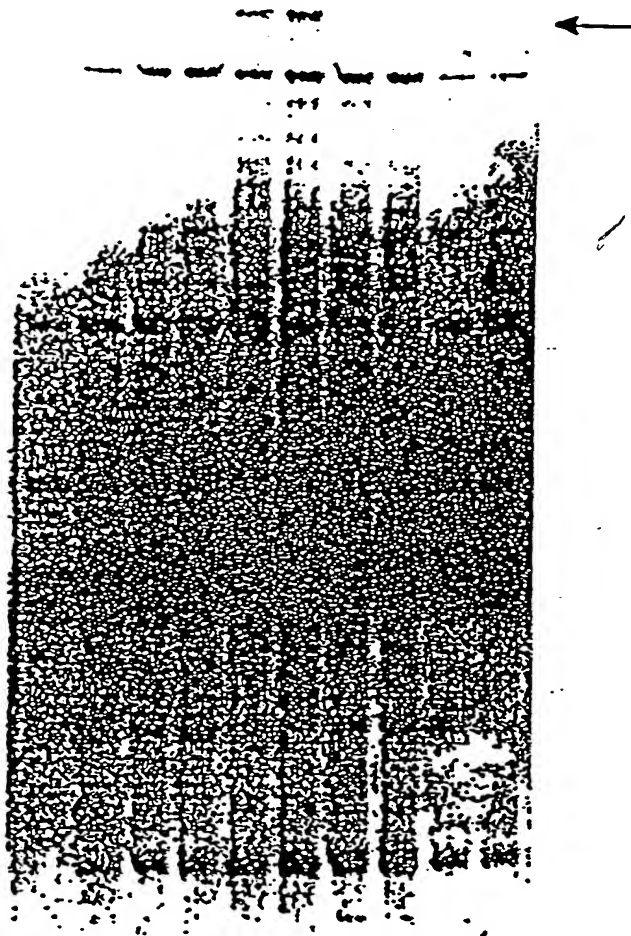


FIG. 1

10004633 120401

10	20	30	40	50	60	
CTGGTGAGGG	GGATCTACAA	CTTGTTTCGGT	TAAAGAAAAA	AGCAACAGCC	AACAGAAATG	60
TGGTTATCCT	TCACCTACCT	AAAAAGGGAG	ATGATGTGAA	ACCAGGAACC	AGATGCCGAG	120
TAGCAGGATG	GGGGAGATTT	GGCAATAAGT	CAGCTCCCTC	TGAAACTCTG	AGAGAAGTCA	180
ACATCACTGT	CATAGACAGA	AAAATCTGCA	ATGATGAAAA	ACACTATAAT	TTTCATCCTG	240
TAATTGGTCT	AAACATGATT	TGGGCAGGGG	ACCTCCCCGG	CGGAAAGGAC	TCCTGCAATG	300
GGGATTCTGG	CAGCCCTCTC	CTATGTGATT	GGTATTTGGG	MGCATCACC	TCCTTTT	357

FIG. 2

10	20	30	40	50	60	
TTAGCGCCAT	TGCCATAGAG	AGACCTCAGC	CATCAATCAC	TAGCACATGA	TTGACAGACA	60
GAGATGTTGA	CTTTGGGCTT	TGGCATTCT	GACACTTCCC	ATGTATTTGA	CAGTTACGGA	120
GGGCAGTAAA	TCGTCCTGGG	GTCTGGAAAA	TGAGGCTTTA	ATTGTGAGAT	GCCCCAAG	180
AGGACGCTCG	ACTTATCCTG	TGGAATGGTA	TTACTCAGAT	ACAAATGAAA	GTATTCCTAC	240
CCAAAAAAAA	AAAAA					255

FIG. 4A

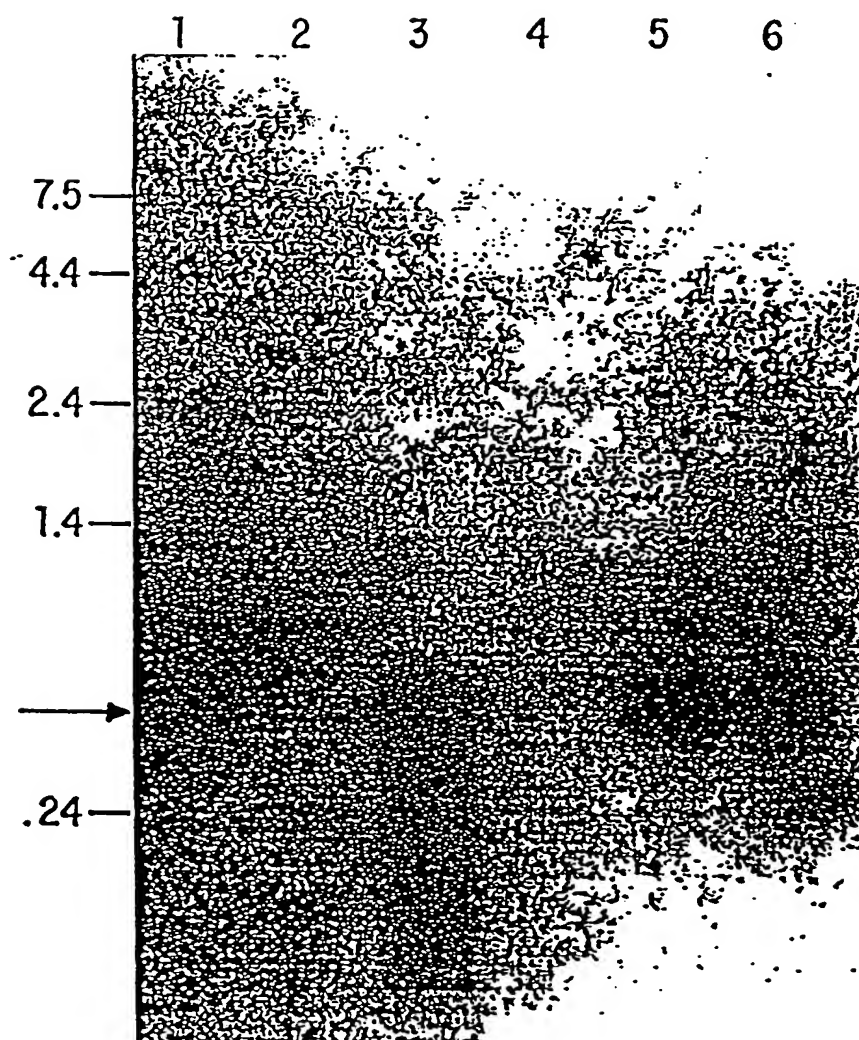


FIG. 3

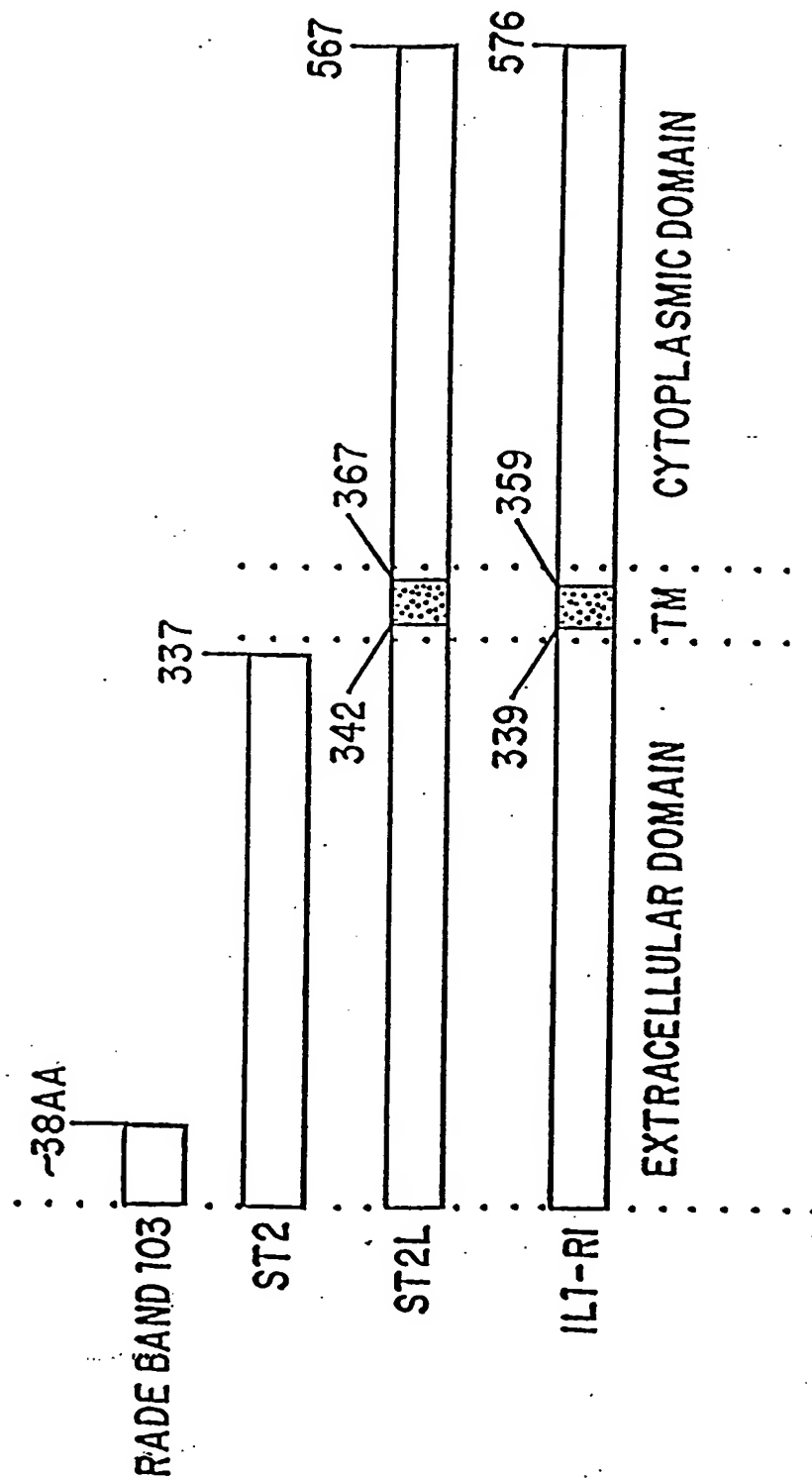


FIG. 4B

1 atgattgaca gacagagaat gggacttgg gctttggcaa ttctgacact tcccatgtat
 61 ttgacagta cggagggcag taaatcgcc tggggtctgg aaaatgaggc ttaattgtg
 121 agatgcccc aaaggagcag ctgacttat cctgtggaat ggtattactc agatacaaat
 181 gaaagtattc ctactcaaaa aagaaatcgg atctttgtct caagagatcg tctgaagttt
 241 ctaccagcca gagtgaaga ctctgggatt tatgcttggt ttatcagaag cccaacttg
 301 aataagactg gatactgaa tgcaccata cataaaaagc cgccaagctg caatatacct
 361 gattatttga tgtactgac agtacgtgga tcagataaaa attcaagat aagctgtcca
 421 acaattgacc tgtataattg gacagcacct gttcagtggt ttaagaactg caaagctctc
 481 caagagccaa gggtcagggc acacagggtcc tactgttca ttgacaactg gactcatgat
 541 gatgaagggtg actacactg tcaattcaca cacgcggaga atggaaccaa ctacatcgtg
 601 acggccacca gatcattcac agttgaagaa aaaggctttt ctatgtttcc agtaattaca
 661 aatcctccat acaaccacac aatggaagtg gaaataggaa aaccagcaag tattgcctgt
 721 tcagcttgct ttggcaaagg ctctcacttc ttggctgatg tcctgtggca gattaacaaa
 781 acagtagttg gaaatttgg tgaagcaaga attcaagaag aggaagggtc aaatgaaagt
 841 tccagcaatg acatggattg ttaacctca gtgttaagga taactgggtg gacagaaaag
 901 gacctgtccc tggaatatga ctgtctggcc ctgaaccttc atggcatgat aaggcacacc
 961 ataaggctga gaaggaaaca accaagtaag gagtgtccct cacacattgc t

FIG. 4C

MIDRQRMGLWALAILTLPMYLTVTEGSKSSWGLENEALIVRCPQRGRSTYPVEWYYSD
 TNESIPTQKRNRIFVSRDRLKFLPARVEDSGIYACVIRSPNLNKTGYLNVTIHKKPPSCNIP
 DYLMYSTVRGSDKNFKITCPTIDLYNWTAPVQWFKNCKALQEPRFRAHRSYLFIDNVTH
 DDEGDYTCQFTHAENGTYIVTATRSFTVEEKGFMSFPVITNPPYNHTMEVEIGKPASIA
 CSACFGKGSHFLADVWLQINKTVVGNFGEARIQEEGRNESSNDMDCLTSVLRITGVT
 EKDLSLEYDCLALNLHGMIRHTIRLRKQPSKECPSHIA

FIG. 4D

10004533-120404

ATGATTGACA	GACAGAGAAT	GGGACTTTGG	GCTTTGGCAA	TTCTGACACT	TCCCATGTAT	60
TTGACAGTTA	CGGAGGGCAG	TAAATCGTCC	TGGGGTCTGG	AAAATGAGGC	TTTAATTGTG	120
AGATGCCCCC	AAAGAGGACG	CTCGACTTAT	CCTGTGGAAT	GGTATTACTC	AGATACAAAT	180
GAAAGTATTC	CTACTCAAAA	AAGAAATCGG	ATCTTTGTCT	CAAGAGATCG	TCTGAAGTTT	240
CTACCAGCCA	GAGTGGGAAG	CTCTGGGATT	TATGCTTGTG	TTATCAGAAG	CCCCAACTTG	300
AATAAGACTG	GATACTTGAA	TGTCACCATA	CATAAAAAAGC	CGCCAAGCTG	CAATATCCCT	360
GATTATTTGA	TGTACTCGAC	AGTACGTGGA	TCAGATAAAA	ATTTCAAGAT	AACGTGTCCA	420
ACAATTGACC	TGTATAATTG	GACAGCACCT	GTTCAGTGGT	TTAAGAACTG	CAAAGCTCTC	480
CAAGAGCCAA	GGTTCAGGGC	ACACAGGTCC	TACTTGTTCA	TTGACAACGT	GACTCATGAT	540
GATGAAGGTG	ACTACACTTG	TCAATTCACA	CACGCGGAGA	ATGGAACCAA	CTACATCGTG	600
ACGGCCACCA	GATCATTCAC	AGTTGAAGAA	AAAGGCTTTT	CTATGTTTCC	AGTAATTACA	660
AATCCTCCAT	ACAACCACAC	AATGGAAGTG	GAAATAGGAA	AACCAGCAAG	TATTGCCTGT	720
TCAGCTTGCT	TTGGCAAAGG	CTCTCACTTC	TTGGCTGATG	TCCTGTGGCA	GATTAACAAA	780
ACAGTAGTTG	GAAATTTTGG	TGAAGCAAGA	ATTCAAGAAG	AGGAAGGTCG	AAATGAAAGT	840
TCCAGCAATG	ACATGGATTG	TTTAACCTCA	GTGTTAAGGA	TAAGTGGTGT	GACAGAAAAG	900
GACCTGTCCC	TGGAATATGA	CTGTCTGGCC	CTGAACCTTC	ATGGCATGAT	AAGGCACACC	960
ATAAGGCTGA	GAAGGAAACA	ACCAATTGAT	CACCGAAGCA	TCTACTACAT	AGTTGCTGGA	1020
TGTAGTTTAT	TGCTAATGTT	TATCAATGTC	TTGGTGATAG	TCTTAAAAGT	GTTCTGGATT	1080
GAGGTTGCTC	TGTTCTGGAG	AGATATAGTG	ACACCTTACA	AAACCCGGAA	CGATGGCAAG	1140
CTCTACGATG	CGTACATCAT	TTACCCTCGG	GTCTTCCGGG	GCAGCGCGGC	GGGAACCCAC	1200
TCTGTGGAGT	ACTTTGTTCA	CCACACTCTG	CCCGACGTTT	TTGAAAATAA	ATGTGGCTAC	1260
AAATTGTGCA	TTTATGGGAG	AGACCTGTTA	CCTGGGCAAG	ATGCAGCCAC	CGTGGTGGAA	1320
AGCAGTATCC	AGAATAGCAG	AAGACAGGTG	TTTGTCTCTG	CCCCTCACAT	GATGCACAGC	1380
AAGGAATTTG	CCTACGAGCA	GGAGATTGCT	CTGCACAGCG	CCCTCATCCA	GAACAACTCC	1440
AAGGTGATTG	TTATTGAAAT	GGAGCCTCTG	GGTGAGGCAA	GCCGACTACA	GGTTGGGGAC	1500
CTGCAAGATT	CTCTCCAGCA	TCTTGTGAAA	ATTCAAGGGA	CCATCAAGTG	GAGGGAAGAT	1560
CATGTGGCCG	ACAAGCAGTC	TCTAAGTTCC	AAATTCTGGA	AGCATGTGAG	GTACCAAATG	1620
CCAGTGCCAG	AAAGAGCCTC	CAAGACGGCA	TCTGTTGCGG	CTCCGTTGAG	TGGCAAGGCA	1680
TGCTTAGACC	TGAAACACTT	TTGA				1704

FIG. 4E

10004633-120401

MIDRQRMGLWALAILTLPMYLTVTEGSKSSWGLENEALIVRCPQRGRSTYPVEWYYSD
TNEIPTQKRNRIFVSRDRLKFLPARVEDSGIYACVIRSPNLNKTGYLNVTIHKKPPSCNIP
DYLMYSTVRGSDKNFKITCPTIDLYNWTAPVQWFKNCKALQEPRFRAHRSYLFIDNVTH
DDEGDYTCQFTHAENGNTNYIVTATRSFTVEEKGFSPVITNPPYNHTMEVEIGKPASIA
CSACFGKGSHFLADVLWQINKTVVGNFGEARIQEEEGRNESSSNDMDCLTSVLRITGVT
EKDLSLEYDCLALNLHGMIRHTIRLRRKQPIDHRSIYYIVAGCSLLLMFINVLVIVLKVFW
IEVALFWRDIVTPYKTRNDGKLYDAYIYPRVFRGSAAGTHSVEYFVHHTLPDVLENKC
GYKLCIYGRDLLPGQDAATVVESSIONSRRQVFLAPHMMHSKEFAYEQEIALHSALIQ
NNSKVILIEMEPLGEASRLQVGDLQDSLQHLVKIQGTIKWREDHVADKQSLSSKFWKHV
RYQMPVPERASKTASVAAPLSGKACLDLKHf

FIG. 4F

FOOTNOTES

1 atcicaacaa cgagttacca atacttgctc ttgattgata aacagaatgg ggTTTTggat
 61 cttagcaatt ctcaaatc tcatgtattc cacagcagca aagtttagta aacaatcatg
 121 gggcctggaa aatgaggctt taattgtaag atgtcctaga caaggaaaac ctagtacac
 181 cgtggattgg tattactcac aaacaaacaa aagtattccc actcaggaaa gaaatcgtgt
 241 gtttgctca ggccaacttc tgaagtttct accagctgaa gttgctgatt ctggtattta
 301 tacctgtatt gtcagaagtc ccacattcaa taggactgga tatgcgaatg tcaccatata
 361 taaaaaacaa tcagattgca atgttcaga ttattgatg tattcaacag tatctggatc
 421 agaaaaaaat tcaaaaattt attgtctac cattgacctc tacaactgga cagcacctct
 481 tgagtgggtt aagaattgtc aggctcttca aggatcaagg tacaggggcg acaagtcatt
 541 ttgggtcatt gataatgtga tgactgagga cgcagggtgat tacacctgta aattatata
 601 caatgaaaat ggagccaatt atagtgtgac ggcgaccagg tccttcacgg tcaaggatga
 661 gcaaggcttt tctctgtttc cagtaatcgg agccccctgca caaatgaaa taaaggaagt
 721 ggaaattgga aaaaacgcaa acctaacttg ctctgcttgt ttggaaaag gcactcagtt
 781 cttggctgcc gtcctgtggc agcttaattg aacaaaaatt acagactttg gtgaaccaag
 841 aattcaacaa gaggaagggc aaatcaaag ttacagcaat gggctggctt gtctagacat
 901 ggttttaaga atagctgacg tgaaggaaga ggatttattg ctgcagtacg actgtctggc
 961 cctgaatttg catggcttga gaaggcacac cgtaagacta agtaggaaaa atccaagtaa
 1021 ggagtgtttc tgagactttg atcacctgaa ctttctctag caagtgaag cagaatggag
 1081 tgtgggtcca agagatccat caagacaatg ggaatggcct gtgccataaa atgtgcttct
 1141 cttctcggg atgtgtttg ctgtctgac tttgtagact gtctctgtt gctgggagct
 1201 tctctgctgc ttaaattgtt cgtctcccc cactccctcc tatcgttggt ttgtctagaa
 1261 cactcagctg cttcttggt catcctgtt tttaacttt atgaactccc tctgtgtcac
 1321 tgtatgtgaa aggaaatgca ccaacaaccg aaaactg

FIG. 4G

MGFWILAILTILMYSTAAKFSKQSWGLENEALIVRCPRQGKPSYTVDWYYSQTNKSIPT
 QERNRVFASGQLLKFLLPAEVADSGIYTCIVRSPTFNRTGYANVTIYKKQSDCNVPDYL
 YSTVSGSEKNSKIYCPTIDL YNWTAPELWFKNCQALQGSRYRAHKSFLVIDNVMTE
 DYTCKFIHNENGANYSVTATRSFTVKDEQGFSLFPVIGAPAQNEIKEVEIGKNANLTCSA
 CFGKGTQFLAAVLWQLNGTKITDFGEPRIQQEQQNQSFNGLACLDMLVRIADVKEED
 LLLQYDCLALNLHGLRRHTVRLSRKNPSKECF

FIG. 4H

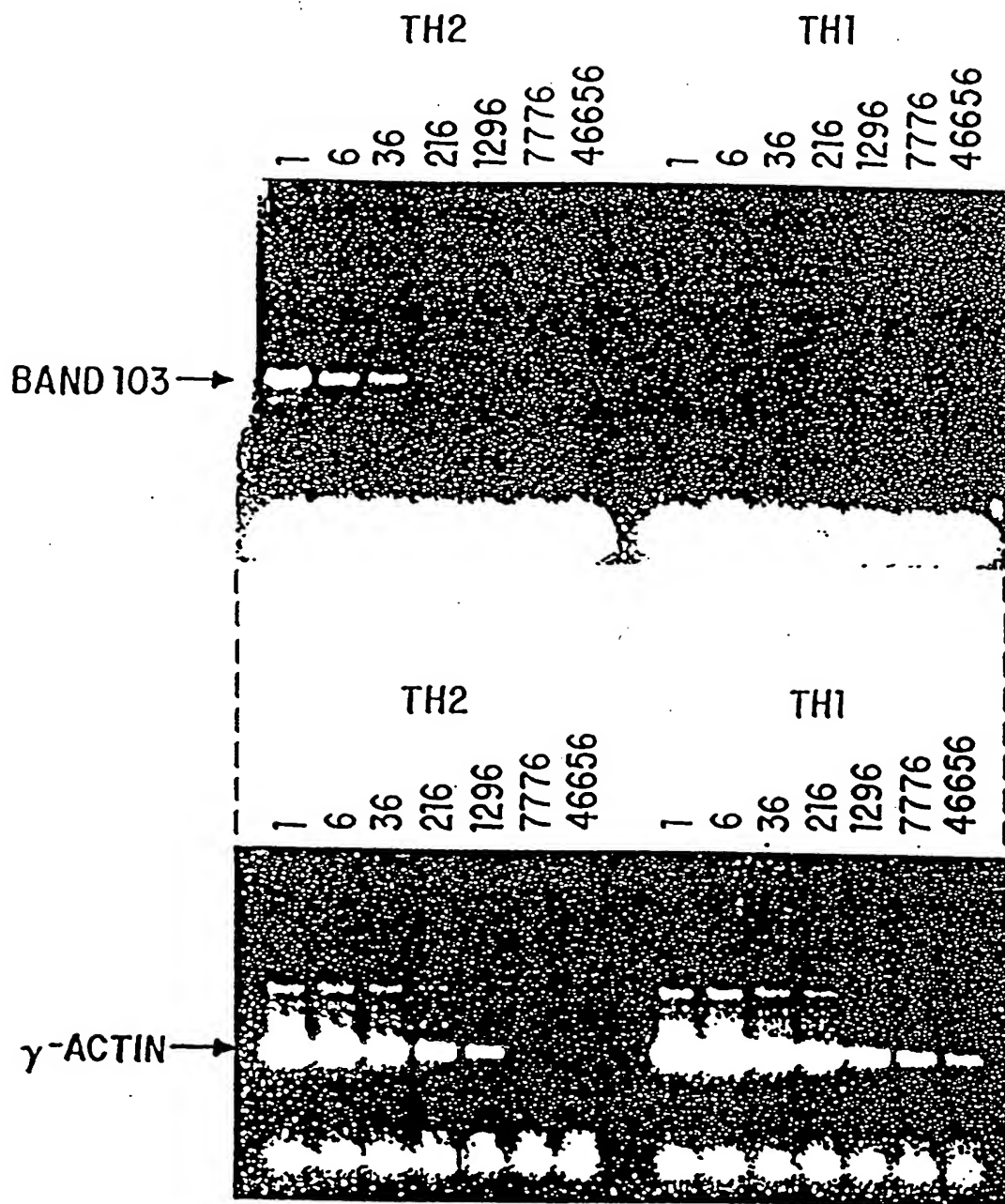


FIG. 5

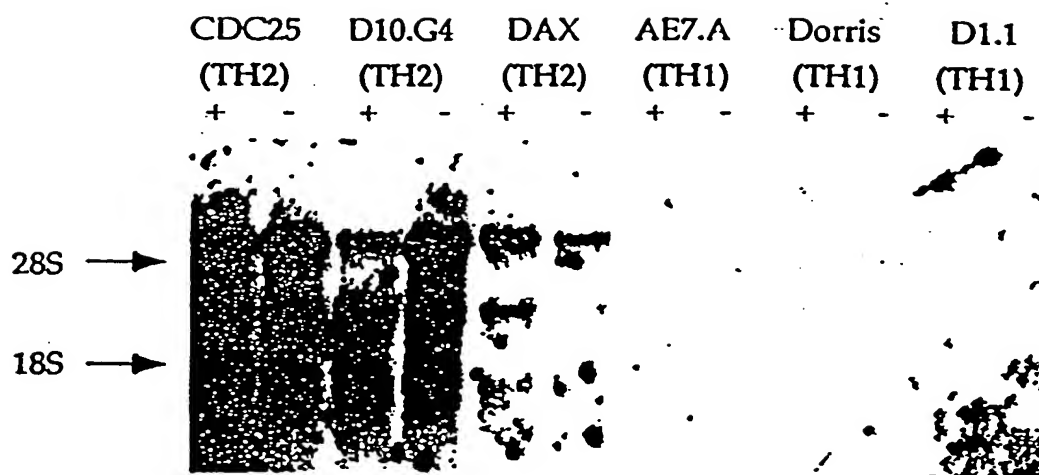


FIG. 6

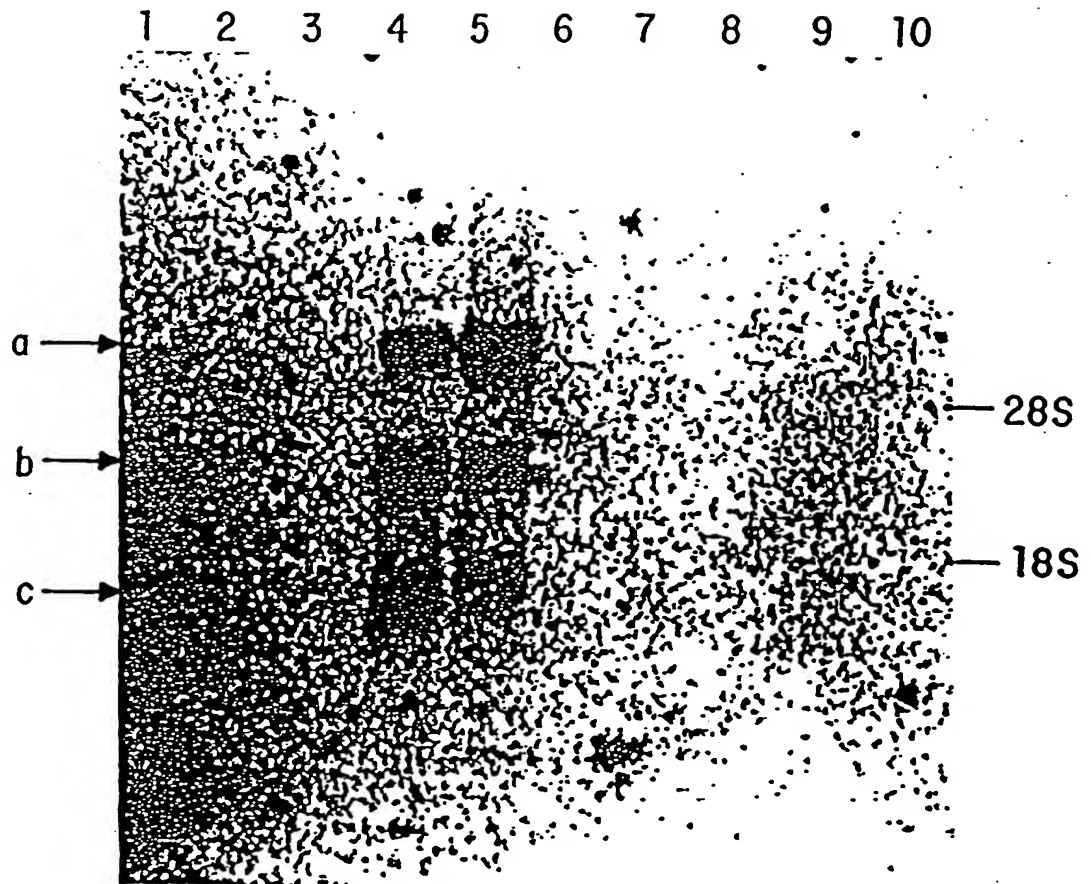


FIG. 7

FOOT" EESHOT

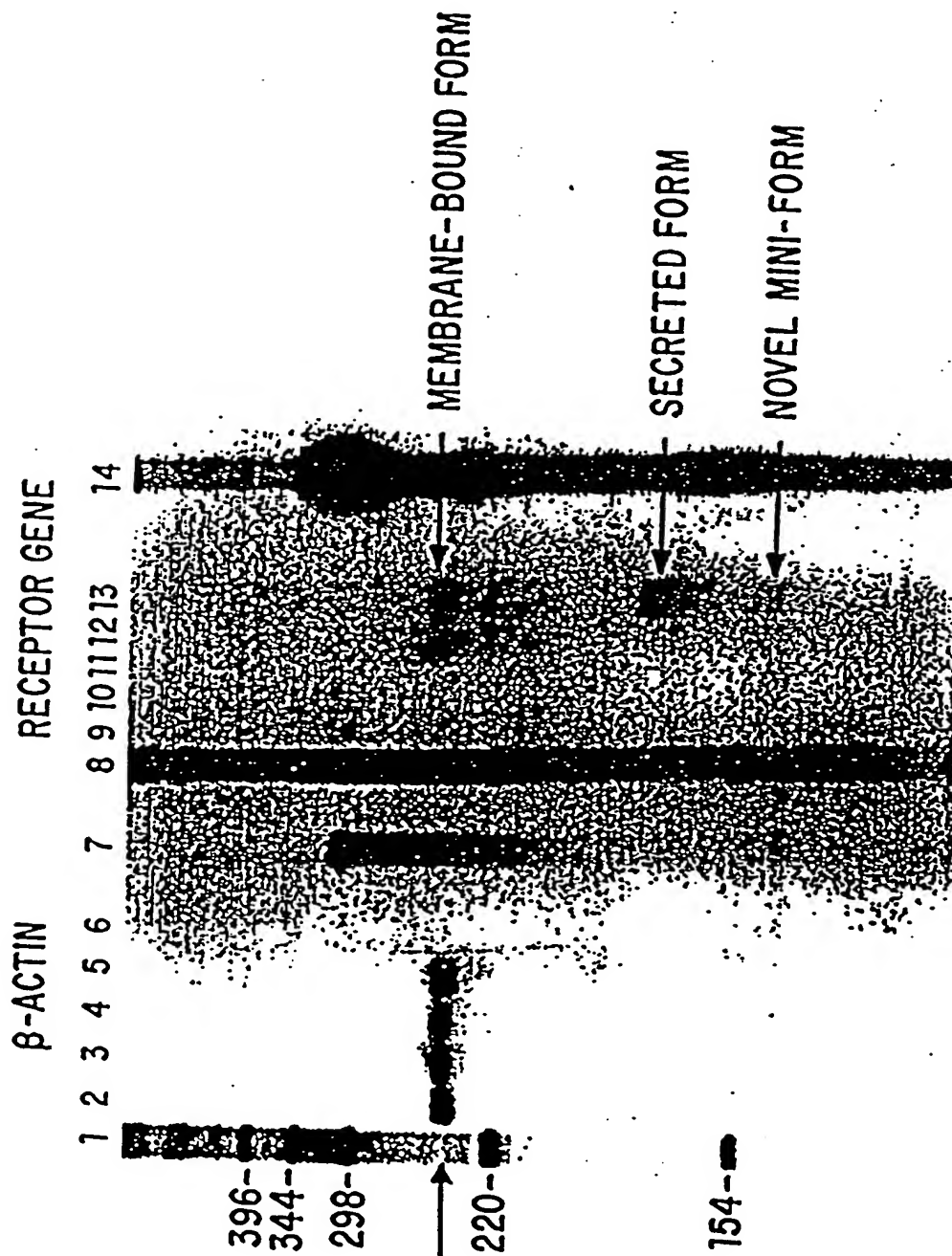


FIG. 8

	CC	2
GGGTGGACCCACGGTCCGAGCCTCCTCAGTCAAGAGAAGCATCCCTCCAGAAACAGGGAACATGACACTTTTGAAAG		81
AATGGCAACGGCGTGAAATAAAACAGAGCATTCCCATTTGCACCGACCAATCTCCAATCTCCTGTAGATTCAAAA		160
GGGCAAGCAAGAGGGCGGTGACCGTTACGAAAGCTAAATCCCATGTATTGAACATGAAGACTTCTGATGCTTAAATC		239
TCATTAACTGCTTTAAGTCACTCCAGGAGCTTGGATCCCAACTTCTAGCAGTAATAGTCTGTGTAAAAA		318
AATCAGTCTACAACCACTCTCTAAATGCATGGATGAACCTCATCAGAACATCAAAACCCAAAGGAACCTAAGAGAGAAG		397
AATTCTAATAAAAGAATTTTACATTGAAAACTTACAAGGCAAGGTCCCTTCCCTGCTGACAGCCTAAGAAGTGATGT		476
	M A M N S M C I E E Q R H L E	15
AACTGCCACTGTGAAGACC ATG GCG ATG AAC AGC ATG TGC ATT GAA GAG CAG CGC CAC CTC GAA		540
H Y L F P V V Y I I V F I V S V P A N I		35
CAC TAT TTG TTC CCG GTG GTC TAC ATA ATT GTG TTT ATA GTC AGC GTC CCA GCC AAC ATC		600
G S L C V S F L Q A K K E N E L G I Y L		55
GGA TCT TTA TGC GTA TCC TTT CTG CAA GCG AAG AAG GAA AAT GAG CTA GGG ATT TAC CTC		660
F S L S L S D L L Y A L T L P L W I N Y		75
TTC AGT CTG TCC CTG TCA GAC CTG CTG TAT GCG CTG ACT CTG CCC CTC TGG ATC AAT TAC		720

FIG. 9A

T W N K D N W T F S P T L C K G S V F F 95
 ACT TGG AAT AAA GAC AAC TGG ACT TTC TCT CCC ACC TTG TGC AAA GGA AGC GTT TTC TTC 780

 T Y M N F Y S S T A F L T C I A L D R Y 115
 ACC TAC ATG AAC TTT TAC AGC AGC ACG GCG TTC CTC ACT TGC ATT GCC CTG GAC CGC TAT 840

 L A V V Y P L K F S F L R T R R F A F I 135
 TTA GCA GTC GTC TAC CCT CTG AAG TTT TCC TTC CTA AGA ACG AGA AGA TTC GCG TTT ATT 900

 T S L S I W I L E S F F N S M L L W K D 155
 ACC AGC CTC TCC ATC TGG ATA TTA GAG TCC TTC TTT AAC TCT ATG CTT CTG TGG AAA GAT 960

 E T S V E Y C D S D K S N F T L C Y D K 175
 GAA ACG AGT GTT GAA TAT TGT GAC TCG GAC AAA TCT AAT TTC ACT CTC TGC TAT GAC AAA 1020

 Y P L E K W Q I N L N L F R T C M G Y A 195
 TAC CCT CTG GAG AAA TGG CAG ATA AAC CTC AAC CTG TTT CGG ACG TGC ATG GGC TAC GCA 1080

 I P L I T I M I C N H K V Y R A V R H N 215
 ATA CCC TTG ATC ACC ATC ATC TGC AAC CAT AAA GTC TAC CGA GCT GTG CGG CAC AAC 1140

 Q A T E N S E K R R I I K L L A S I T L 235
 CAA GCC ACG GAA AAC AGC GAG AAG AGA AGG ATC ATA AAG TTG CTT GCT ACG ATC ACG TTG 1200

 T F V L C F T P F H V M V L I R C V L E 255
 ACT TJC GTC CTA TGC TTT ACC CCC TTC CAC GTG ATG GTG CTC ATC CGC TGC GTT TTA GAG 1260

FIG. 9B

R D M N V N D K S G W Q T F T V Y R V T 275
CGC GAC ATG AAC GTC AAT GAC AAG TCT GGA TGG CAG ACG TTT ACG GTG TAC AGA GTC ACA 1320

V A L T S L N C V A D P I L Y C F V T E 295
GTA GCC CTG ACG AGT CTA AAC TGT GTT GCC GAT CCC ATT CTG TAC TGC TTT GTG ACT GAG 1380

T G R A D M W N I L K L C T R K H N R H 315
ACG GGG AGA GCT GAT ATG TGG AAC ATA TTA AAA TTG TGT ACT AGG AAA CAC AAT AGA CAC 1440

Q G K K R D I L S V S T R D A V E L E I 335
 CAA GGG AAA AAA AGG GAC ATA CTT TCT GTG TCC ACA AGA GAT GCT GTA GAA TTA GAG ATT 1500

I D * 338
 ATA GAC TAA GAGGTGGAGGCAGGTTAAGTTACATGGTATTATTAAATGAACTTACATTTTGGAAAAGAAATCTGG 1576

CATAGTAGAACCCAGTGGAAATAGTTGAAGGTACATTGTATGACTCCTATGTGGCTTTATTAAAGTAAGGTATAGAAA 1655

TGTAATTATCTTGATGTATTCTAATGACTAGGCATCATTTGTTTAGTACCAATTCTCTTTGCCCTCTATGTTATAACCCC 1734

TAAGAAGCAGCGGGACTGTTGCTCTTTAAATCAGTGGCCATTCTATCTGACTACTATGACTTTTTTGTGTTGTTCTGC 1813

TTTGGGTTTTCAGTCTGCCCTGCATCAGTCTTCTCCTCTGTATACGTCGTCTTCAACAAATGTAAGGACTAAATACCCC 1892

FIG. 9C

TCCGGATCACATCCATTATCAAGGATTTGAAGCCACTCCATGTACTGGGTTATAAAGAAATGTTCTCATGAACTTTCA 1971

TGAAGTTACATACCTTTGGGGATCTAGTCACCGAGTCACATAAAGTAAATGGAAAAA 2050

AGGc

FIG. 9D

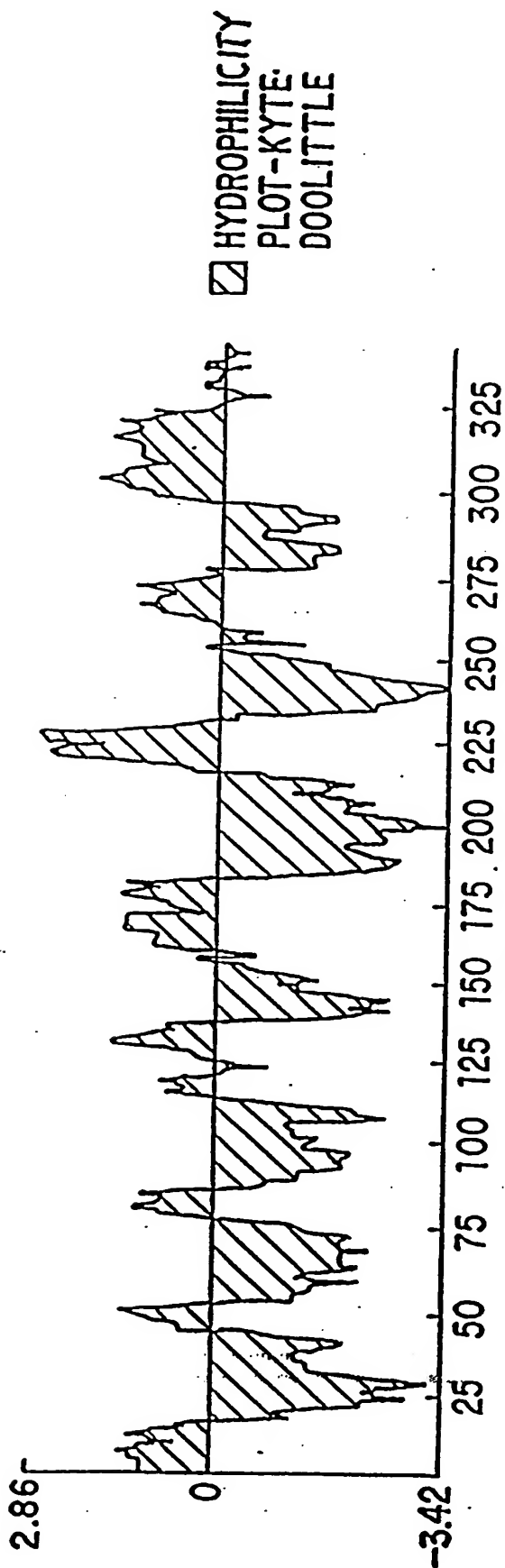


FIG. 10A

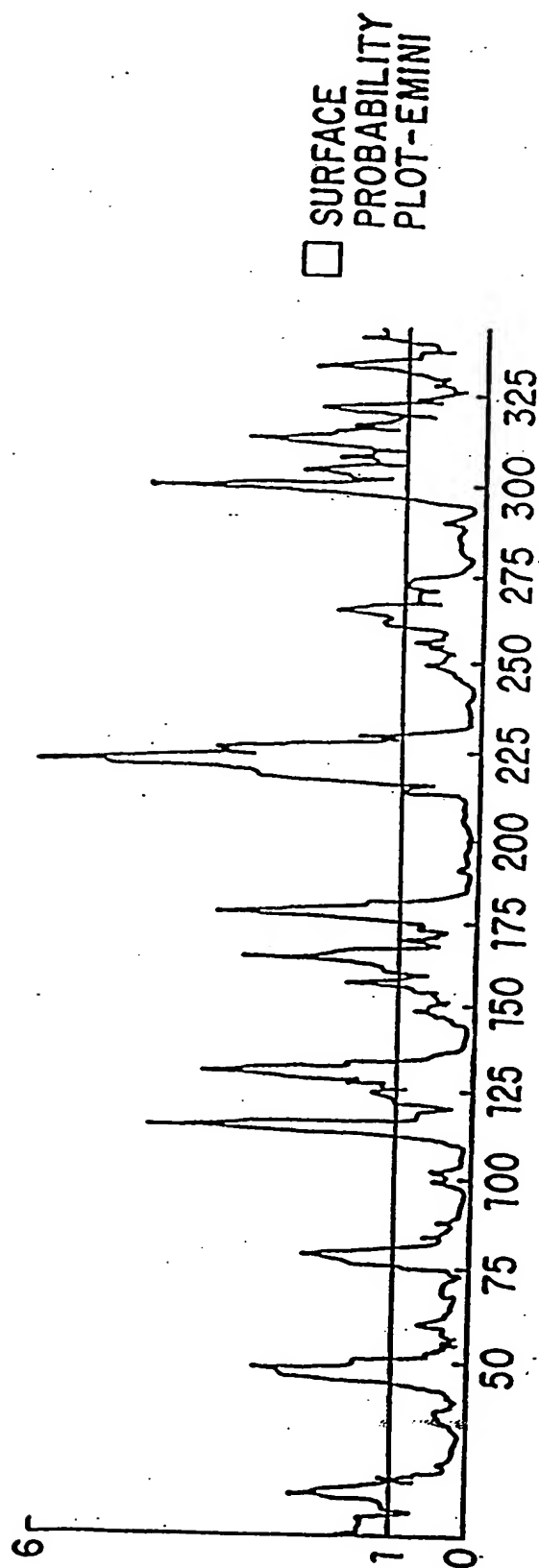


FIG. 10B

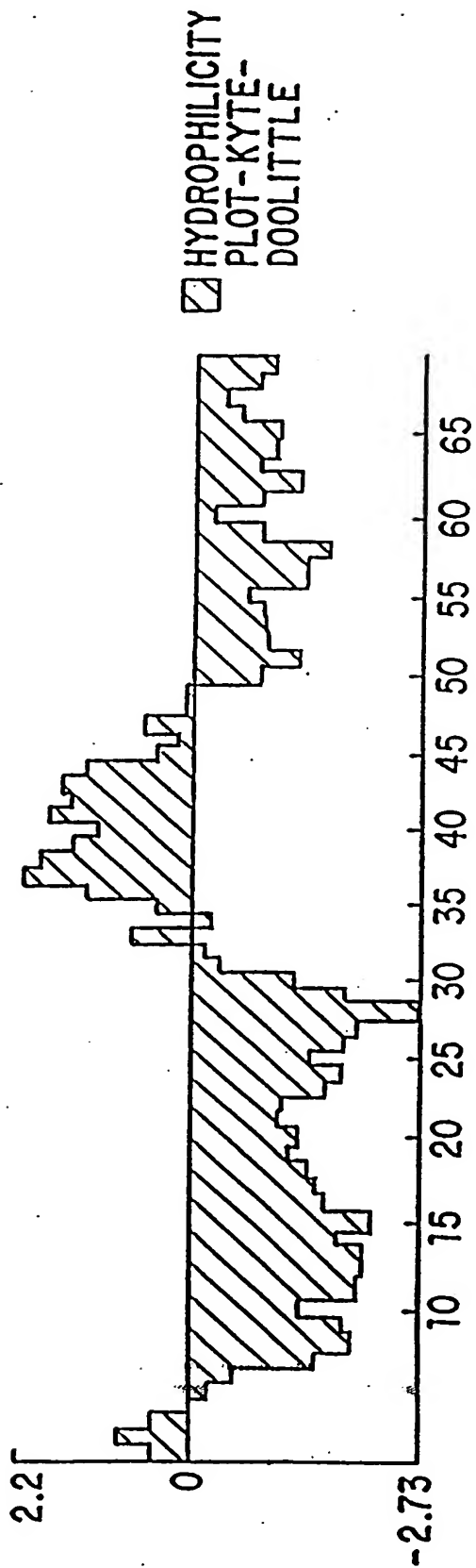


FIG. 10C

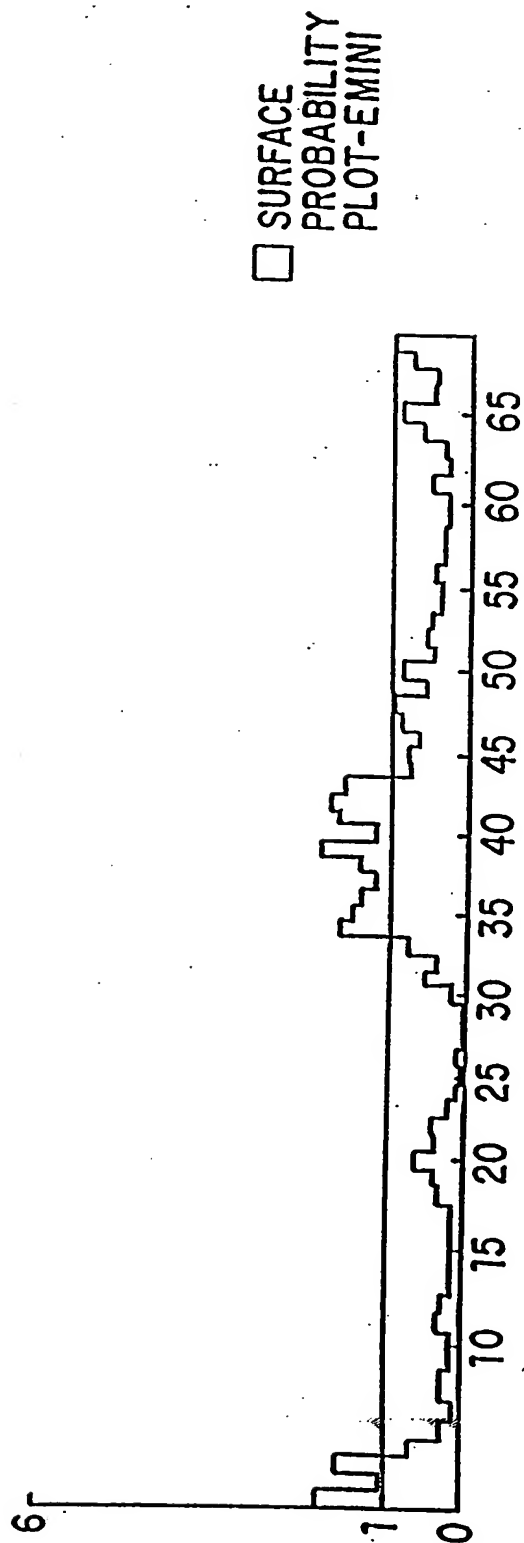


FIG. 10D

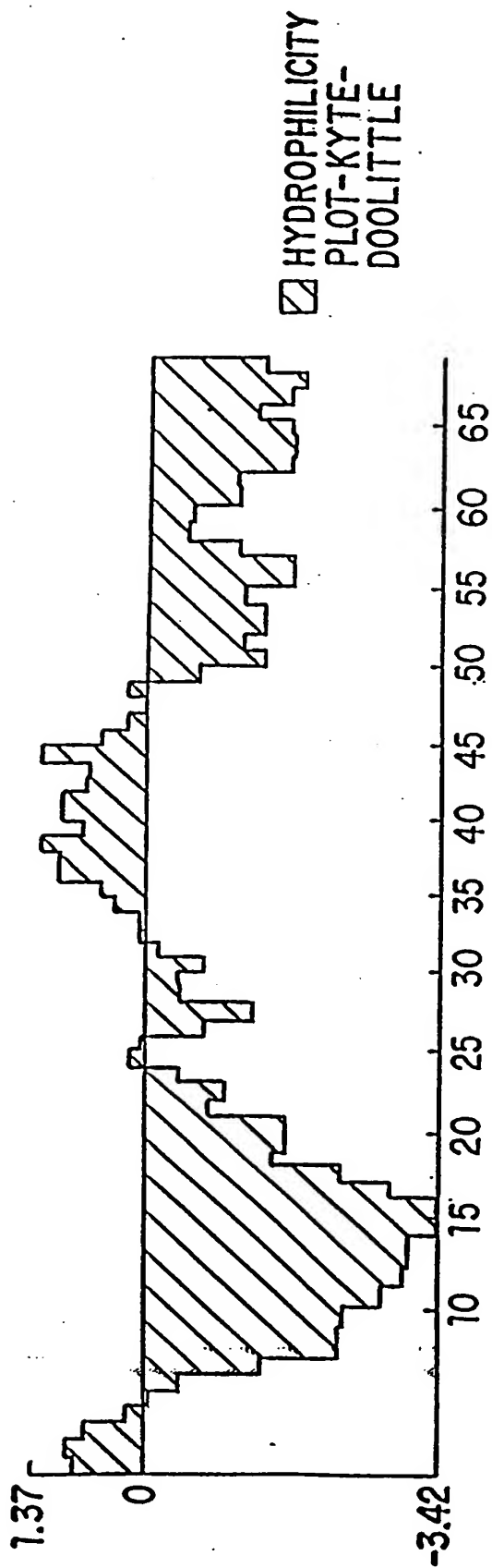


FIG. 10E

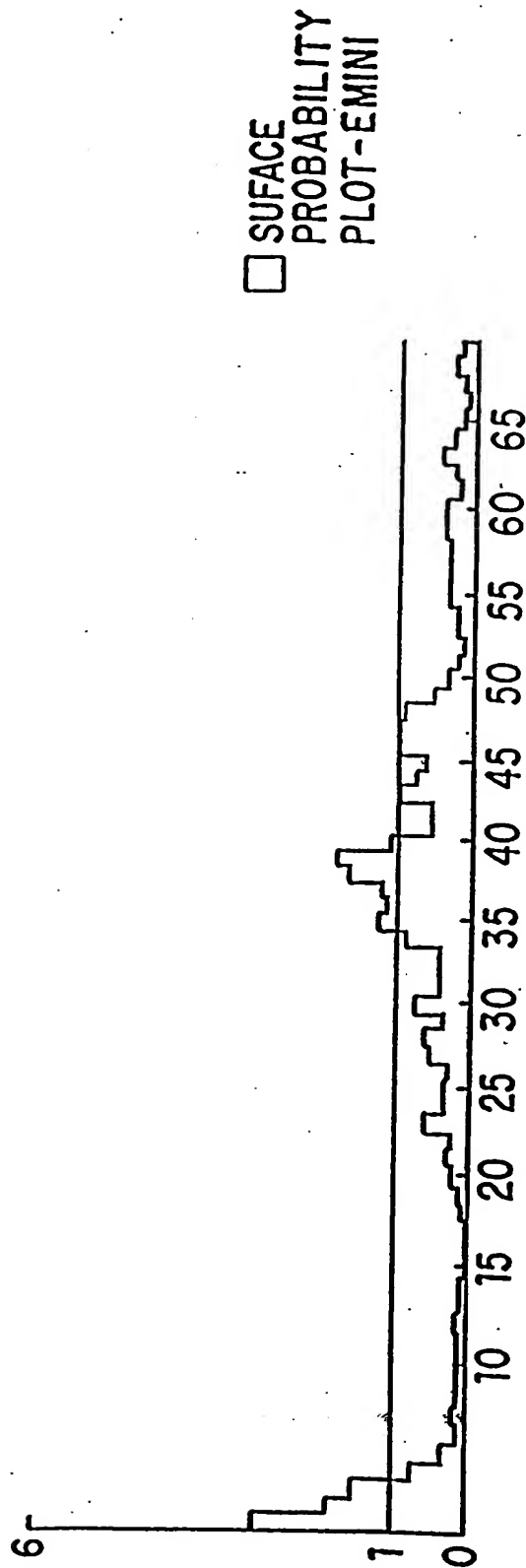


FIG. 10F

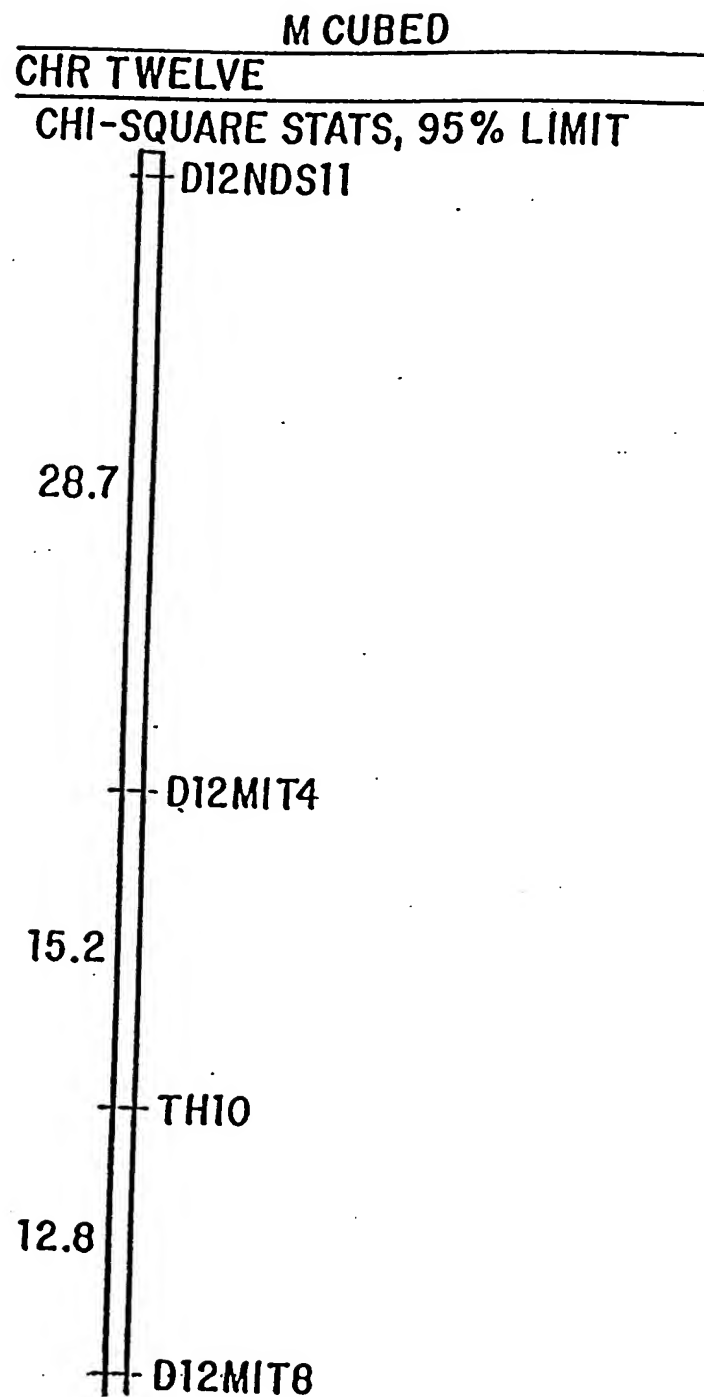


FIG. 11

10004633-120401

CGCCAGTGTGCTGGAATTCGGCTTAGAGCATTTCCTTCA
AACCAAGGTTACACACACTTACTAAAAGCAATGCTG
TTAGAGGAGAAGGGCTTGGGAGACTCGGCCATTTGAAAC
ANAAGCAAGGCACTCTCCAGGNNCAGCAAGTGGATTCCC
ATTTCTGCTGAGGGCGGGTTCACACTGAGACTGCACTC
CAGTCAGCGGGAGGAATCACCTGCATTAATGCTTGTCT
CTGCAGAGCTAGTGTGCCTTCCACTCTGGGTACACTTGG
GTGTCAACATTTCAAATGATGACCTAAGAGGCTCTCAT
AGTTGGTGATACTATGGNAGGACAGAGAACACTGGCT
GTATTGTCTTTTTCTTTCAGCACTAGTGTCTTGGCCCTT
AATAAACGGGTTCCATCATCTCCAACAGGAGAT
AGATTGTTAGACAGGTCTTTCCCCCTCACT

FIG. 12

TTTNNGGGACAGGGTTTCNCTGTGTATCTCTGGCTGTCC
TGGAACNACTCTGTAGACCAGGTTGGCCTCGANCTCAG
AAATCTACCTGCCTCTCCCTCCANAGTGCTGGGATTAA
GGTGTATGCCACCAATNCCCGGCCTTAATATATTNNTAA
ACAACTTCATTTGAATGANATATTGACACTACCCTTGG
ATAAGAGTNCCCAGAATGANGTACAGGNTTCANGGAATC
ATTAA

FIG. 14

CTTAGCAGGTGGAGTTGCAGCAGGAAGCCTGGTAGCCAC
ACTCCAATCAGCAGGGGTCTTGGACTCTCCACATCAAC
AAATGCCATCCTAGGGGCTGCTGGGGCACTGTTGGAGCC
TTGCTCTGAGCTTAGGAGATGACACTTCTATCAGCTCA
CTCAAAGCCTGTACAGACTACGCAGGAGATGAAGTTCCA
AAAGGCACCTTCAGAACCTCA

FIG. 15

10 20 30 40 50 60 70
TTTTTTTTT TNGGAGAGG CTAGCACTGA AATTACAGTT TCAGTGGAA TTAGAGAAGT AATAACTGCA 70
AAAATTTTATT TACACACACA CACACACACA CAGGGCATT TACCTGTGTA AGTGCAGTTT AATCANCCCC 140
ATTACCTTAT GACCTTGGT GGCAATGTCT CTAAGCTTT AAAATTAAAA TAAATTAAA AGATGGTTT 210
TCCATCTCAT AAAATCCCCT TTGGGAATGG AAGACTTCCT CTTTGGGGTN TTTTGTAGAG GGAACAGGAG 280
GTAACGTGTA ATTATTTATA CATTCTAATA AACCATGAAT GCACCACATA AAATACTGTA CTCGGGGAGC 350
AAACACTGTN TGGGGGGGTT CTCTCTTACC AGAAGGAACA GGGGGCTTTT CAATGGCTGT GGGC 414

FIG. 13

7853-125

(SHEET 23 OF 47)

remt161g0f	F-----		BAND 161
g1/218574/	MRQKAVSLFLCYLLLLFTCSGVEAGKKKCESSESDSGSF-WKALTFMAVGGGLAVAGLP--	CHIMP	GENE
g1/32698/g	MRQKAVSVFLCYLLLLFTCSGVEAGKKKCESSESDSGSF-WKALTFMAVGGGLAVAGLP--	HUMAN	6-16
g1/32701/g	-----VEAGKKKCESSESDSGSF-WKALTFMAVGGGLAVAGLP--	HUMAN	6-16
g1/32702/g	-----GKKKCESSESDSGSF-WKALTFMAVGGGLAVAGLP--	HUMAN	6-16
g1/35184/g	MEASAL-----TSSAVTSVAKVVRVASGSVVLPLARIATVWIGGVVMAAAMPV	HUMAN	P27
remt161g0f	---FVFLA-----GGVAAGSLVATLQSGVLGLSTSTNAILGAA	BAND 161	
g1/218574/	--ALGFTGAGIAANSVAASLMSWSAILNGGVPAGGLVATLQSLGAGG-----SSVITGNI	CHIMP	GENE
g1/32698/g	--ALGFTGAGIAANSVAASLMSWSAILNGGVPAGGLVATLQSLGAGG-----SSVITGNI	HUMAN	6-16
g1/32701/g	--ALGFTGAGIAANSVAASLMSWSAILNGGVPAGGLVATLQSLGAGG-----SSVITGNI	HUMAN	6-16
g1/32702/g	--ALGFTGAGIAANSVAASLMSWSAILNGGVPAGGLVATLQSLGAGG-----SSVITGNI	HUMAN	6-16
g1/35184/g	LSAMGFTAAGIASSSIAAKMMSAAAIANGGVSAGSLVGTLSGLTKFILGSI	HUMAN	P27
remt161g0f	GALLEPCSELRR-----	BAND 161	
g1/218574/	GALMGYATHKYLDSEEDDEE	CHIMP	GENE
g1/32698/g	GALMRYATHKYLDSEEDDEE	HUMAN	6-16
g1/32701/g	GALMRYATHKYLDSEEDDEE	HUMAN	6-16
g1/32702/g	GALMRYATHKYLDSEEDDEE	HUMAN	6-16
g1/35184/g	GSAIAAVIARFY	HUMAN	P27

FIG. 16

NGTCGACCCACGGTCGGATTCCCTCCCAAGTACTC ATG TTT TCA GGT CTT ACC CTC 60
 M F S G L T L 6
 N C V L L L Q L L L A R S L E D G Y K 26
 AAC TGT GTC CTG CTG CAA CTA CTA CTT GCA AGG TCA TTG GAA GAT GGT TAT AAG 120
 V E V G K N A Y L P C S Y T L P T S G T 46
 GTT GAG GTT GGT AAA AAT GCC TAT CTG CCC TGC AGT TAC ACT CTA CCT ACA TCT GGG ACA 180
 L V P M C W G K G F C P W S Q C T N E L 66
 CTT GTG CCT ATG TGC TGG GGC AAG GGA TTC TGT CCT TGG TCA CAG TGT ACC AAT GAG TTG 240
 L R T D E R N V T Y Q K S S R Y Q L K G 86
 CTC AGA ACT GAT GAA AGA AAT GTG ACA TAT CAG AAA TCC AGC AGA TAC CAG CTA AAG GGC 300
 D L N K G D V S L I I K N V T L D D H G 106
 GAT CTC AAC AAA GGA GAT GTG TCT CTG ATC ATA AAG AAT GTG ACT CTG GAT GAC CAT GGG 360
 T Y C C R I Q F P G L M N D K K L E L K 126
 ACC TAC TGC TGC AGG ATA CAG TTC CCT GGT CTT ATG AAT GAT AAA AAA TTA GAA CTG AAA 420
 L D I K A A K V T P A Q T A H G D S T T 146
 TTA GAC ATC AAA GCA GCC AAG GTC ACT CCA GCT CAG ACT GCC CAT GGG GAC TCT ACT ACA 480
 A S P R T L T T E R N G S E T Q T L V T 166
 GCT TGT CCA AGA ACC CTA ACC ACG GAG AGA AAT GGT TCA GAG ACA CAG ACA CTG GTG ACC 540

FIG. 17A

L H N N N G T K I S T W A D E I K D S G 186
 CTC CAT AAT AAC AAT GGA ACA AAA ATT TCC ACA TGG GCT GAT GAA ATT AAG GAC TCT GGA 600

 E T I R T A I H I G V G V S A G L T L A 206
 GAA ACG ATC AGA ACT GCT ATC CAC ATT GGA GTG GGA GTC TCT GCT GGG TTG ACC CTG GCA 660

 L I I G V L I L K W Y S C K K K L S S 226
 CTT ATC ATT GGT GTC TTA ATC CTT AAA TGG TAT TCC TGT AAG AAA AAG AAG TTA TCG AGT 720

 L S L I T L A N L P P G G L A N A G A V 246
 TTG AGC CTT ATT ACA CTG GCC AAC TTG CCT CCA GGA GGG TTG GCA AAT GCA GGA GCA GTC 780

 R I R S E E N I Y T I E E N V Y E V E N 266
 AGG ATT CGC TCT GAG GAA AAT ATC TAC ACC ATC GAG GAG AAC GTA TAT GAA GTG GAG AAT 840

 S N E Y Y C Y V N S Q Q P S * 280
 TCA AAT GAG TAC TAC TGC TAC GTC AAC AGC CAG CAG CCA TCC TGA CCGCCTCTGGACTGCCACT 903

 TTTAAGGCTGGCCTTCATTTCTGACTTTGGTATTTCCCTTTKTGGAAACTATGTGATATGTCACTTGGCAACCTCAT 982

 TGGAGGTTCTGACCACAGCCACTGAGAAAAGAGTCCAGTTTTCTGGGGATAATTAACTACAAGGGGATTCGACTGTA 1061

 ACTCATGCTACATTGAAATGCTCCATTTATCCCTGAGTTTCAGGGATCGGATCTCCCACTCCAGAGACTTCAATCATG 1140

 CGTGTGAAGCTCACTCGTGCTTTCATACATTAGGAATGGTAGTGATGCTTTTGAGACATAGAGGTTTGTGGTATA 1219

FIG. 17B

TCCGCAAAAGCTCCTGAAAGGTAGGGGGAATAAAGGGCTAAGATAGGAAGGTGCGGYTCTTTGTTGATGTTGGAAAAATC 1298
TTAAAGAAGTTGGTAGCTTTTCT AGAGATTTTCTGACCTTGAAAGATTAAGAAAAAGCCAGGTGGCATATGCTTAACAC 1376
GATATAACTTTGGGAACCTTAGGCAGGAGGGTGATAAGTTCAAGTCAAGTCAGCCAGGGCTATGCTGGTAAGACTGTCTCAMEA 1455
TCCAAGACGAAAAATAAACATAGAGACAGCAGGAGGGCTGGAGATGAGGCTCGGACAGTGAGGTGCATTGTGTACAAGCA 1534
CGAGGAATCTATATTTGATCGTAGACCCACATGAAAAAGCTAGGCCTGGTAGAGCATGCTTGTAGACTCAAGAGATGG 1613
AGAGGTAAAGGCACAACAGATCCCCGGGGCTTGGGTGCAGTCAGCTTAGCCTAGGTGCTGAGTTCCAAGTCCACAAGAG 1692
TGCTGTCTCAMAGTAAGATGGRCTGAGTATCTGGCGCATGTCCATGGGGGTTGTCTCTCCTCTCAGAAGAGACATGC 1771
ACATGACCCCTGCACACACACACACACACACACACACACACACACACATGAAATGAAGGTTCTCTCTG 1850
TGCTGTACCTCTCTATAACATGTATCTACAGGACTCTCCTCTGCCTCTGTTAAGACATGAGTGGGAGCATGGCAG 1929
AGCAGTCCAGTAATTTATTCAGCACTCAGAAGGCTGGAGCAGAAGCGTGGAGAGTTCAGGAGCACTGTGCCCCAACACT 2008
GCCAGACTCTTTACACAAGAAAAAGGTTACCCGCAAGCAGCCTGCTGTCTGTAAAGGAAACCCCTGCGAAAGGCAAA 2087
CTTGACTGTTGTGTGCTCAAGGGGAAGTACTCAGACAACTTCTCCATTCTCTGGAGGAAACTGGAGCTGTTTCTGACA 2166
GAAGAACAACCGGTGACTGGGACATACGAAGGCAGAGCTCTTGAGCAATCTATATAGTCAGCAAAATATCTTTGGGA 2245

FIG. 17C

GGACAGTCGTACCAAAATTGATTTCCAGCCGGTGGACCTCAGTTTCATCTGGCTTACAGCTGCCAGTGCCCTT 2324
 GATCTGTGCTGGCTCCCATCTATAACAGAATCAAAATTAATAGACCCCGAGTGAAAAATTAAGTGAGCAGAAAGGTAG 2403
 CTTTGTTCAAAGATTTTTTGCATTGGGGAGCAACTGTGTACATCAGAGGACATCTGTTAGTGAGGACACCAAAACCTG 2482
 TGGTACCGTTTTTTCATGTATGAATTTTGTGTTAGGTTGCTTCTAGCTAGCTGTGGAGGTCTGGCTTTCTTAGGTG 2561
 GGTATGGAAGGGAGACCATCTAACAAAAATCCATTAGAGATAACAGCTCTCATGCAGAGGGAAAACTAATCTCAAATGT 2640
 TTTAAAGTAATAAACTGTACTGGCAAAGTACTTTGAGCATAAAAAAGGGGGGGCGC 2710

FIG. 17D

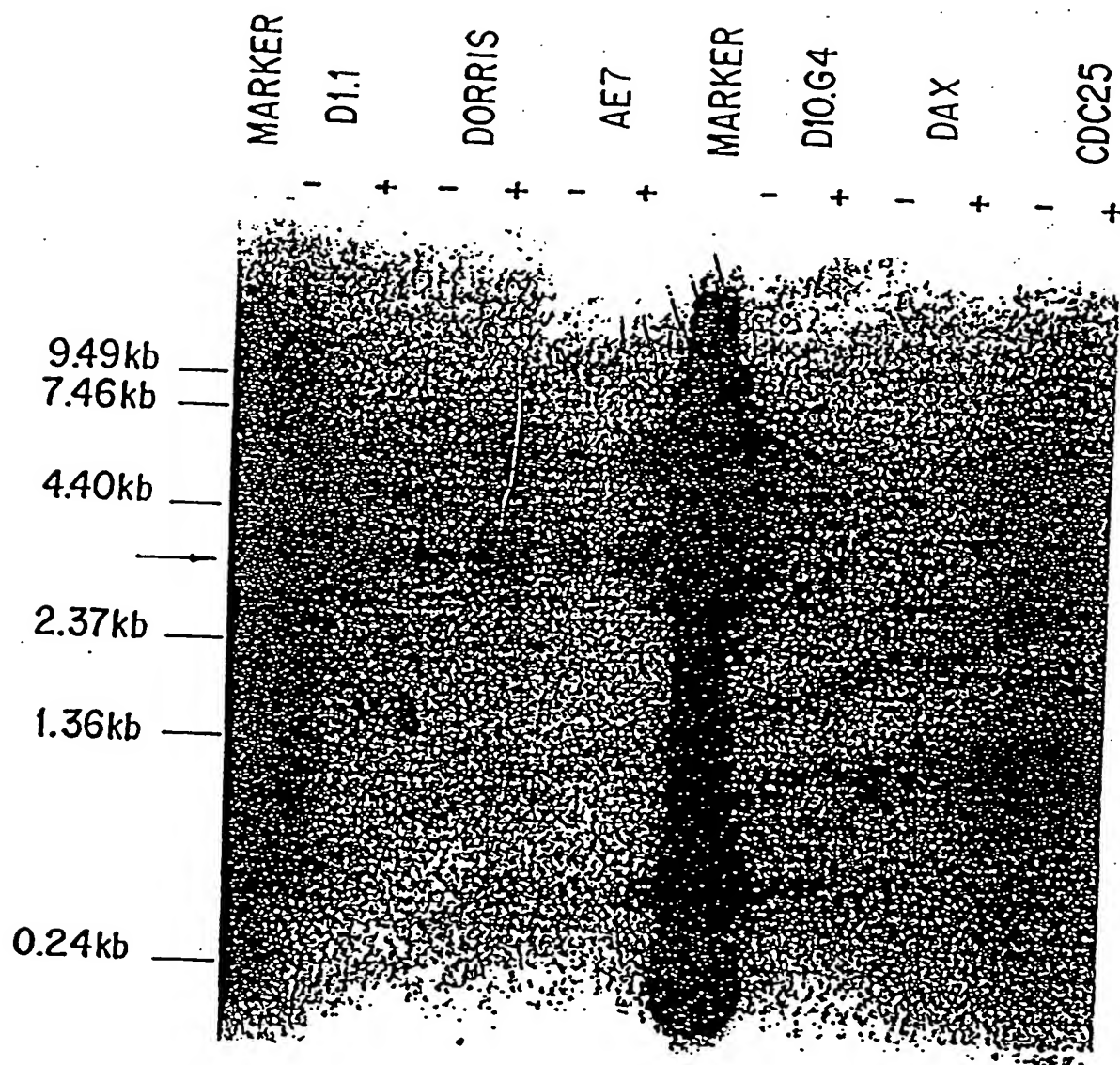


FIG. 18

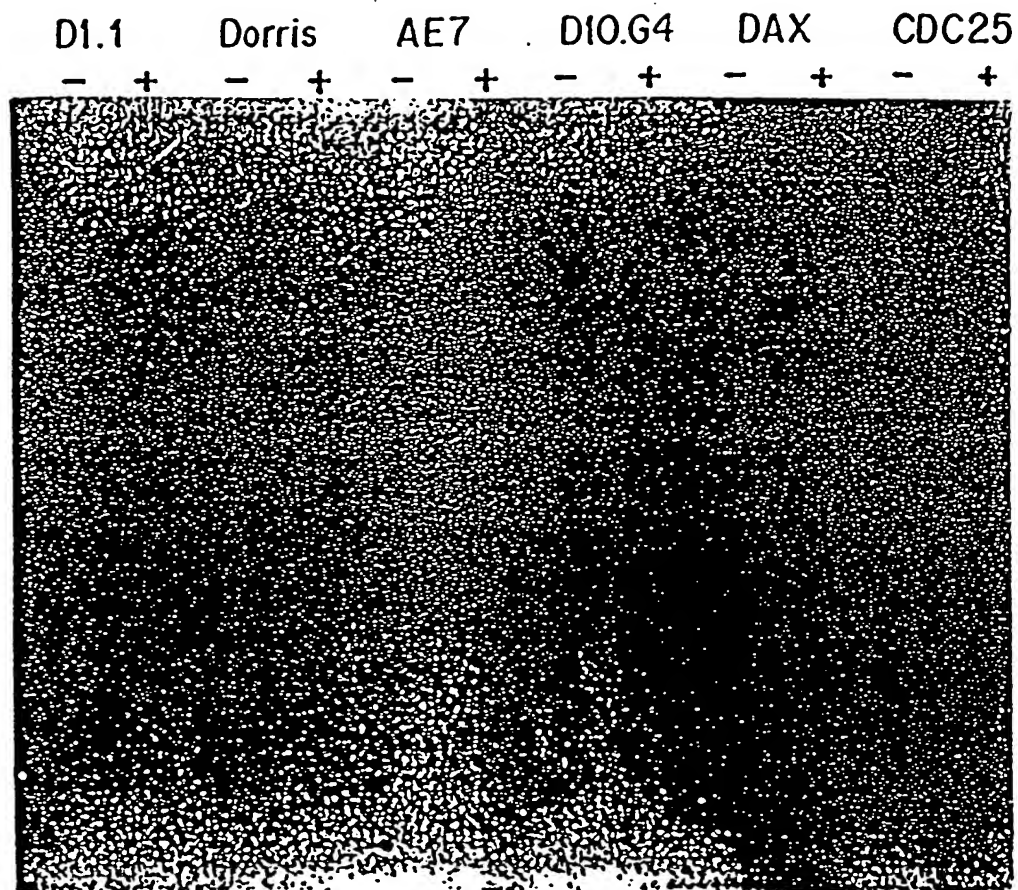


FIG. 19

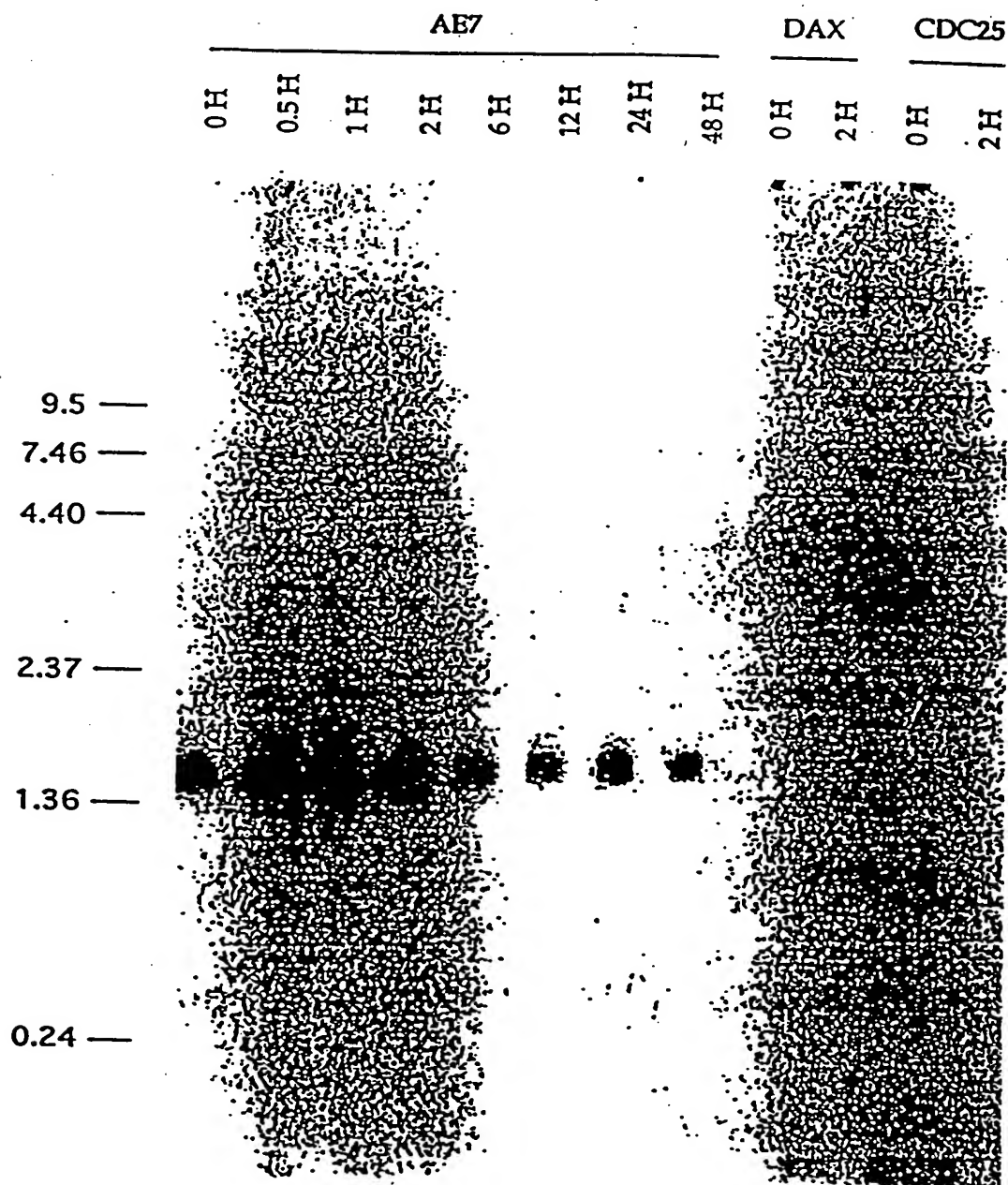


FIG. 20

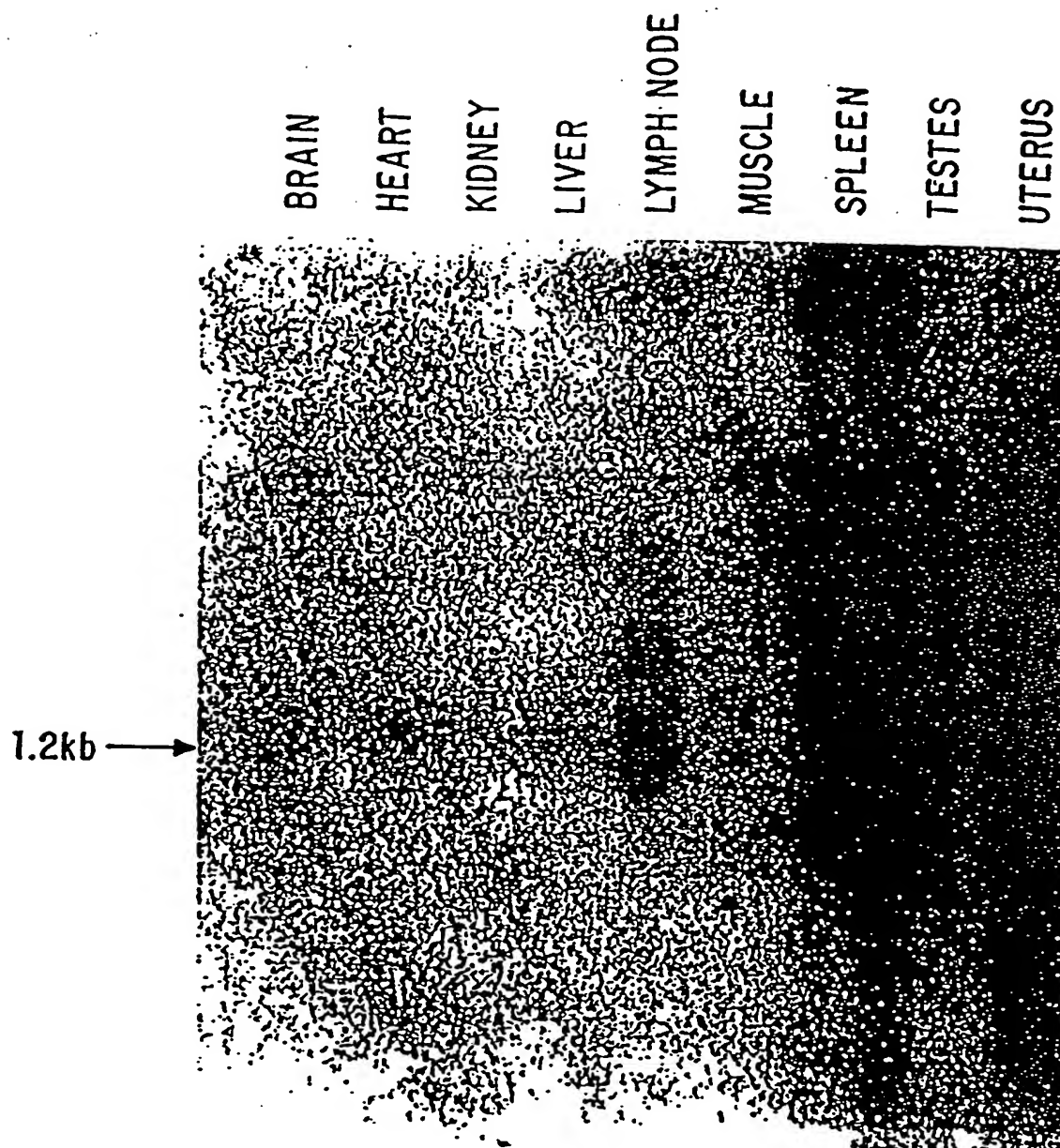


FIG. 21

C CGGGTCGACC CACGGTCCG ATG ACA CTG ACT GCC CAC CTC TCC TAC TTT CTG GTC CTG 13
 60
 L L A G Q G L S D S L L T K D A G P R P 33
 TTG TTA GCG GGC CAA GGC CTC AGT GAC TCC CTC CTC ACC AAG GAT GCA GGT CCC CGC CCA 120
 L E L K E V F K L F Q I R F N R S Y W N 53
 CTG GAG CTG AAG GAA GTC TTC AAG CTG TTC CAG ATC CGG TTC AAC CGG AGT TAC TGG AAC 180
 P A E Y T R L S I F A H N L A Q A Q R 73
 CCA GCA GAG TAC ACT CGC CGT CTG AGC ATC TTT GCC CAC AAT CTG GCT CAG GCT CAA AGG 240
 L Q Q E D L G T A E F G E T P F S D L T 93
 CTA CAG CAA GAA GAC TTG GGT ACA GCT GAG TTT GGA GAG ACT CCA TTC AGT GAC CTC ACA 300
 E E F G Q L Y G Q E R S P E R T P N M 113
 GAG GAG GAG TTT GGC CAG TTA TAC GGG CAG GAG AGG TCA CCA GAA AGG ACC CCC AAC ATG 360
 T K K V E S N T W G E S V P R T C D W R 133
 ACC AAA AAG GTA GAG TCT AAC ACG TGG GGG GAA TCT GTG CCC CGC ACC TGT GAC TGG CGT 420
 K A K N I I S S V K N Q G S C K C W A 153
 AAA GCA AAG AAC ATC TCG TCG GTC AAG AAC CAG GGA AGC TGC AAA TGC TGC TGG GCC 480
 M A A A D N I Q A L W R I K H Q Q F V D 173
 ATG GCA GCT GCC GAC AAC ATC CAG GCT CTG TGG CGC ATC AAA CAC CAG TTT GTG GAC 540

FIG. 22A

V S V Q E L L D C E R C G N G C N G G F 193
 GTG TCT GTG CAG GAG CTG CTG GAC TGC GAA CGC TGT GGA AAT GGT TGC AAT GGT GGC TTC 600

V W D A Y L T V L N N S G -L A S E K D Y 213
 GTG TGG GAC GCA TAT CTA ACT GTC CTC AAC AAC AGT GGC CTG GCC AGT GAA AAG GAT TAT 660

P F Q G D R K P H R C L A K K Y K K V A 233
 CCA TTC CAG GGG GAC AGA AAG CCT CAC AGA TGC CTA GCC AAG AAG TAC AAG AAG GTG GCC 720

W I Q D F T M L S N N E Q A I A H Y L A 253
 TGG ATC CAG GAT TTC ACC ATG TTG TCC AAT AAT GAG CAG GCA ATT GCC CAC TAC CTG GCC 780

V H G P I T V T I N M K L L Q H Y Q K G 273
 GTG CAT GGA CCT ATC ACC GTG ACC ATC AAC ATG AAA CTA CTC CAG CAT TAC CAG AAG GGT 840

V I K A T P S S C D P R Q V D H S V L L 293
 GTC ATC AAG GCT ACA CCC AGC TCC TGT GAC CCT CGG CAA GTG GAC CAC TCT GTC TTG CTG 900

V G F G K E K E G M Q T G T V L S H S R 313
 GTG GGC TTT GGC AAG GAG AAA GAG GGC ATG CAG ACA GGG ACA GTC TTG TCC CAT TCT CGA 960

K R R H S S P Y W I L K N S W G A H W G 333
 AAA CGT CGC CAC TCC TCC CCA TAC TGG ATC CTG AAG AAC TCC TGG GGA GCT CAC TGG GGC 1020

E K G Y F R L Y R G N N T C G V T K Y P 353
 GAG AAG GGT TAC TTC AGG CTG TAT CGG GGA AAC AAC ACC TGT GGA GTC ACC AAG TAT CCC 1080

FIG. 22B

TGGCTTCATA AACCAAGACT GCTCCGTGAA AAAAAAAAAAAAAA

F T A Q V D S P V K K A R T S C P P * 371
TTC ACA GCT CAA GTG GAC TCA CCA GTA AAG AAG GCA CGG ACC TCT TGT CCT CCC TGA AGG 1140
CAGCAGVCAC TCTTCTGCTT CTCCACATG GCCACTGCCC CTTGTCAGCC CTGCCCCACAT CCTCTCTGTA 1210
TGGCTTCATA AACCAAGACT GCTCCGTGAA AAAAAAAAAAAAAA 1257

FIG. 22C

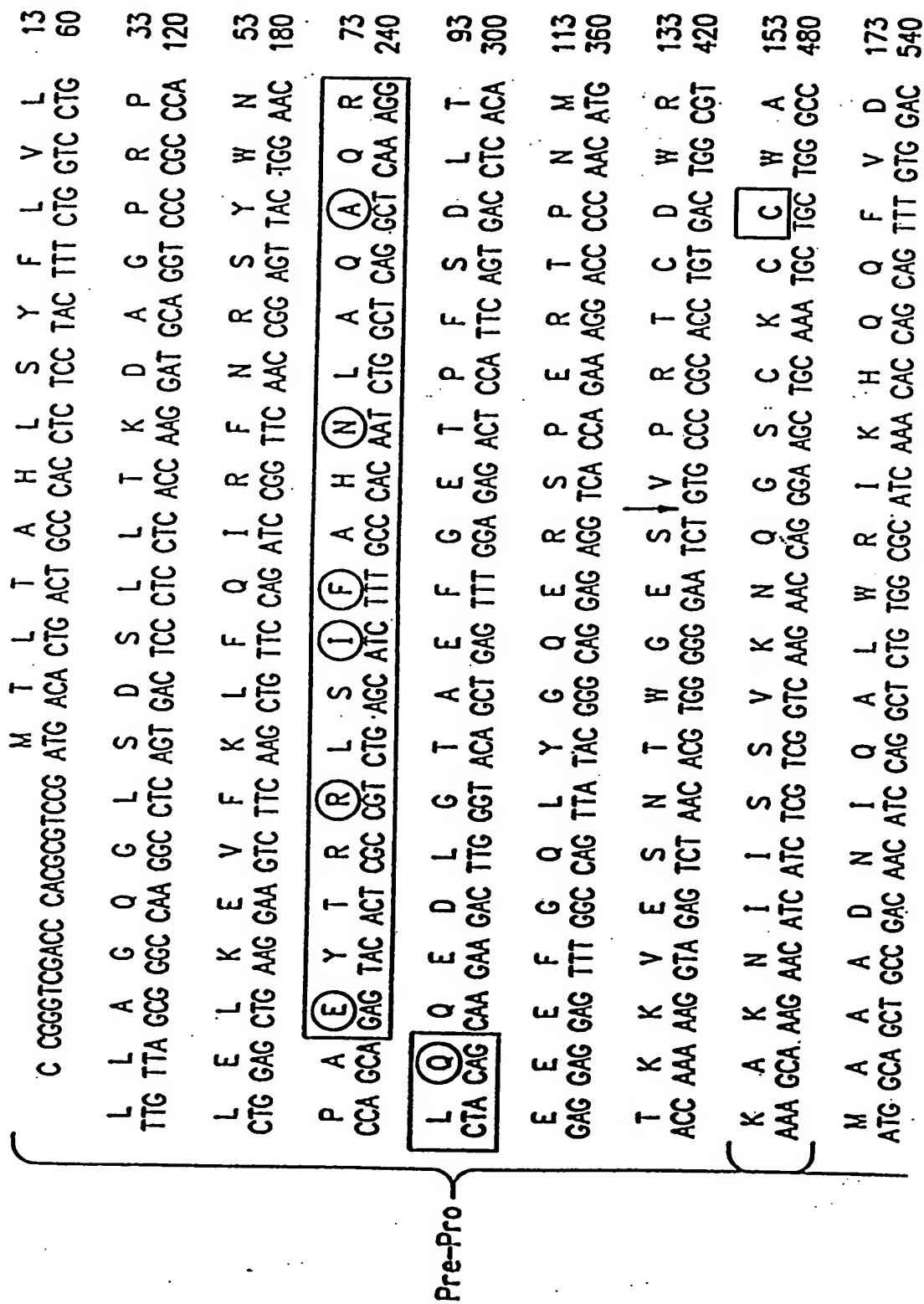


FIG. 23A

V	S	V	Q	E	L	L	D	C	E	R	C	G	N	G	C	N	G	C	F	193
GTC	TCT	GTG	CAG	GAG	CTG	CTG	GAC	TGC	GAA	CGC	TGT	GGA	AAT	GGT	TGC	AAT	GGT	GGC	TTC	600
V	W	D	A	Y	L	T	V	L	N	S	G	L	A	S	E	K	D	Y	213	
GTG	TGG	GAC	GCA	TAT	CTA	ACT	GTC	CTC	AAC	AAC	AGT	GCC	CTG	GCC	AGT	GAA	AAG	GAT	TAT	660
P	F	Q	G	D	R	K	P	H	R	C	L	A	K	K	Y	K	K	V	A	233
CCA	TTC	CAG	GGG	GAC	AGA	AAG	CCT	CAC	AGA	TGC	CTA	GCC	AAG	AAG	TAC	AAG	AAG	GTG	GCC	720
W	I	Q	D	F	T	M	L	S	N	N	E	Q	A	I	A	H	Y	L	A	253
TGG	ATC	CAG	GAT	TTC	ACC	ATG	TTG	TCC	AAT	AAT	GAG	CAG	GCA	ATT	GCC	CAC	TAC	CTG	GCC	780
V	H	G	P	I	T	V	T	I	N	M	K	L	L	Q	H	Y	Q	K	G	273
GTG	CAT	GGA	CCT	ATC	ACC	GTG	ACC	ATC	AAC	ATG	AAA	CTA	CTC	CAG	CAT	TAC	CAG	AAG	GGT	840
V	I	K	A	T	P	S	S	C	D	P	R	Q	V	D	H	S	V	L	L	293
GTC	ATC	AAG	GCT	ACA	CCC	AGC	TCC	TGT	GAC	CCT	CGG	CAA	GTG	GAC	CAC	TCT	GTC	TTG	CTG	900
V	G	F	G	K	E	K	E	G	M	Q	T	G	T	V	L	S	H	S	R	313
GTG	GGC	TTT	GGC	AAG	GAG	AAA	GAG	GGC	ATG	CAG	ACA	GGG	ACA	GTC	TTG	TCC	CAT	TCT	CGA	960
K	R	R	H	S	S	P	Y	W	I	L	K	N	S	W	G	A	H	W	G	333
AAA	CGT	CGC	CAC	TCC	TCC	CCA	TAC	TGG	ATC	CTG	AAG	AAC	TCC	TGG	GGA	GCT	CAC	TGG	GGC	1020

MATURE

FIG. 23B

E	K	G	Y	F	R	L	Y	R	G	N	N	T	C	G	V	T	K	Y	P	353
GAG	AAG	GGT	TAC	TTC	AGG	CTG	TAT	CGG	GGA	AAC	AAC	ACC	TGT	GGA	GTC	ACC	AAG	TAT	CCC	1080
F	T	A	Q	V	D	S	P	V	K	K	A	R	T	S	C	P	P	*		371
TTC	ACA	GCT	CAA	GTG	GAC	TCA	CCA	GTA	AAG	AAG	GCA	CGG	ACC	TCT	TGT	CCT	CCC	TGA	AGG	1140
CAGCAGVCAC TCTTCTGCTT CTCCACATG GCCACTGCC CTTGTCAGCC CTGCCACAT CCTCTCTGTA 1210																				
TGGCTTCATA AACCAAGACT GCTCCGTGAA AAAAAAAAAAAAAA 1257																				

FIG.23C

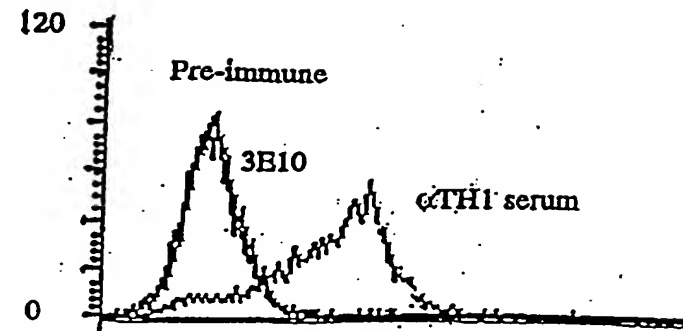
CGCTAACAGAGGTGTCTCTGACTTTTCTTCTGCAAGCTOC																		M	F	S	H	L	P	6
																		ATG	TTT	TCA	CAT	CTT	CCC	18
F	D	C	V	L	L	L	L	L	L	L	L	T	R	S	S	E	V	E	Y	26				
TTT	GAC	TGT	GTC	CTG	CTG	CTG	CTG	CTA	CTA	CTT	ACA	AGG	TCC	TCA	GAA	GTG	GAA	TAC	78					
R	A	E	V	G	Q	N	A	Y	L	P	C	F	Y	T	P	A	A	P	G	46				
AGA	GCG	GAG	GTC	GGT	CAG	AAT	GCC	TAT	CTG	CCC	TGC	TTC	TAC	ACC	CCA	GCC	GCC	CCA	GGG	138				
N	L	V	P	V	C	W	G	K	G	A	C	P	V	F	E	C	G	N	V	66				
AAC	CTC	GTG	CCC	GTG	TGC	TGG	GGC	AAA	GGA	GCC	TGT	CCT	GTG	TTT	GAA	TGT	GGC	AAC	GTG	198				
V	L	R	T	D	E	R	D	V	N	Y	W	T	S	R	Y	W	L	N	G	86				
GTG	CTC	AGG	ACT	GAT	GAA	AGG	GAT	GTG	AAT	TAT	TGG	ACA	TCC	AGA	TAC	TGG	CTA	AAT	GGG	258				
D	F	R	K	G	D	V	S	L	T	I	E	N	V	T	L	A	D	S	G	106				
GAT	TTC	CGC	AAA	GGA	GAT	GTG	TCC	CTG	ACC	ATA	GAG	AAT	GTG	ACT	CTA	GCA	GAC	AGT	GGG	318				
I	Y	C	C	R	I	Q	I	P	G	I	M	N	D	E	K	F	N	L	K	126				
ATC	TAC	TGC	TGC	CGG	ATC	CAA	ATC	CCA	GGC	ATA	ATG	AAT	GAT	GAA	AAA	TTT	AAC	CTG	AAG	378				
L	V	I	K	P	A	K	V	T	P	A	P	T	L	Q	R	D	F	T	A	146				
TTG	GTC	ATC	AAA	CCA	GCC	AAG	GTC	ACC	CCT	GCA	CCG	ACT	CTG	CAG	AGA	GAC	TTC	ACT	GCA	438				
A	F	P	R	M	L	T	T	R	G	H	G	P	A	E	T	Q	T	L	G	166				
GCC	TTT	CCA	AGG	ATG	CTT	ACC	ACC	AGG	GGA	CAT	GGC	CCA	GCA	GAG	ACA	CAG	ACA	CTG	GGG	498				
S	L	P	D	I	N	L	T	Q	I	S	T	L	A	N	E	L	R	D	S	186				
AGC	CTC	CCT	GAT	ATA	AAT	CTA	ACA	CAA	ATA	TCC	ACA	TTG	GCC	AAT	GAG	TTA	CGG	GAC	TCT	558				
R	L	A	N	D	L	R	D	S	G	A	T	I	R	I	G	I	Y	I	G	206				
AGA	TTG	GCC	AAT	GAC	TTA	CGG	GAC	TCT	GGA	GCA	ACC	ATC	AGA	ATA	GGC	ATC	TAC	ATC	GGA	618				
A	G	I	C	A	G	L	A	L	A	L	I	F	G	A	L	I	F	K	W	226				
GCA	GGG	ATC	TGT	GCT	GGG	CTG	GCT	CTG	GCT	CTT	ATC	TTC	GGC	GCT	TTA	ATT	TTC	AAA	TGG	678				
Y	S	H	S	K	E	K	I	Q	N	L	S	L	I	S	L	A	N	L	P	246				
TAT	TCT	CAT	AGC	AAA	GAG	AAG	ATA	CAG	AAT	TTA	AGC	CTC	ATC	TCT	TTG	GCC	AAC	CTC	CCT	738				
P	S	G	L	A	N	A	V	A	E	G	I	R	S	E	E	N	I	Y	T	266				
CCC	TCA	GGA	TTG	GCA	AAT	GCA	GTA	GCA	GAG	GGA	ATT	CGC	TCA	GAA	GAA	AAC	ATC	TAT	ACC	798				
I	E	E	N	V	Y	E	V	E	E	P	N	E	Y	Y	C	Y	V	S	S	286				
ATT	GAA	GAG	AAC	GTA	TAT	GAA	GTG	GAG	GAG	CCC	AAT	GAG	TAT	TAT	TGC	TAT	GTC	AGC	AGC	858				
R	Q	Q	P	S	Q	P	L	G	C	R	F	A	M	P						301				
AGG	CAG	CAA	CCC	TCA	CAA	CCT	TTG	GGT	TGT	CGC	TTT	GCA	ATG	CCA	TAGAT	CAACCA	COCTTAT			903				
TTTGAGCTTGGTGTGTTTGTCTTTTTCAGAACTATGAGCTGTGTCAOCTGACTGGTTTTTGAGGTTCTGTGCACTGCTA																								
TGGAGCAGAGTTTTCCCATTTTTCAGAAGATAATGACTCAGATGGGAATTGAACTGGGAOCTGCACTGAACTTAAACAGG																								
CATGTCAATGCOCTCTGTATTTAAGOCACAGAGTTAOCACACOCAGAGACTGTTAATCATGGATGTTAGAGCTCAAAAG																								
GGCTTTTATATACACTAGGAATTTCTGAAGTGGGGTCTCTGAGAGCTOCAGGAAATTOGGG CACATCATATGTGOCATGA																								
AACTTCAGATAAACTAGGAAAACTGGGTCTGAGGTGAAAGCATAACCTTTTTTGGCACAGAAAGTCTAAAGGGGOCAC																								
TGATTTTCAAAGAGATCTGTGATCOCTTTTTGTGTTTTTGTGTTTTGAGATGGAGTCTGTCTCTGTTGCOCCAGGCTGGAGT																								
GCAATGGCACAATCTOGGCTCACTGCAAGCTCOGCOCTOCTGGGTTCAAGOGATTCTOCTGCOCTCAGCOCTOCTGAGTGGC																								
TGGGATTACAGGCATGCAOCCACCATGCOCCAGCTAATTTGTTGTATTTTGTAGTAGAGACAGGTTTCAOCCATGTTGGCCA																								

GTGTGGTCTCAAACCTCCTGAOCTCATGATTGGCTGGCTGGGCTOCCAAAGCAGTGGGATTACAGGGGTGAGCCACCA
CATCCAGCCAGTGATCCTTAAAGATTAAAGATGACTGGACTAGGTCTAOCCTGATCTTGAAGATTCCCTTGGAAATGT
TGAGATTTAGGCTTATTTGAGCACTACCTGCCCACCTGTCAGTGCCAGTGCATAGCCCTTCTTTTGTCTOCTTATGAA
GACTGCOOCTGCAGGGCTGAGATGTGGCAGGAGCTOCCAGGGAAGGAAGTGCATTTGATTGGTGTGTATTGGCCAAG
TTTTGCTTGTGTGTGTGCTTGAAAGAAAATATCTCTGAOCAACTTCTGTATTGGTGGACAAACTGAAGCTATATTTTTC
ACAGAAGAAGAAGCAGTGAAGGGACACAAATCTGTTCCTGGTGGAAAGAAGGCAAAGGCTTCAGCAATCTATATT
ACCAGGGCTGGATCCTTTGACAGAGAGTGGTCCCTAAACTTAAATTTCAAGACGGTATAGGCTTGATCTGTCTTGCTTA
TTGTGGCCCCCTGGCCCTAGCACAATTCTGACACACAATTGGAACCTACTAAAAATTTTTTTTACTGTAAAAA
AAAAA

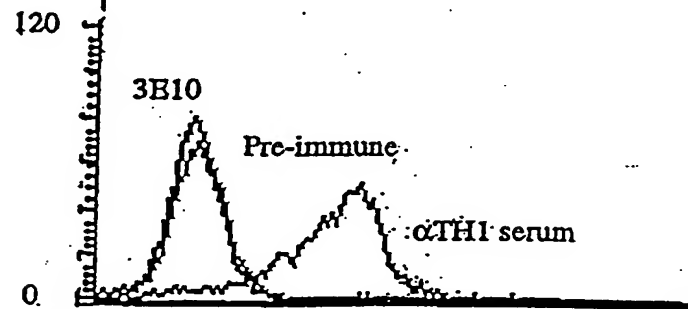
FIG. 24 (cont'd.)

10004633-120401

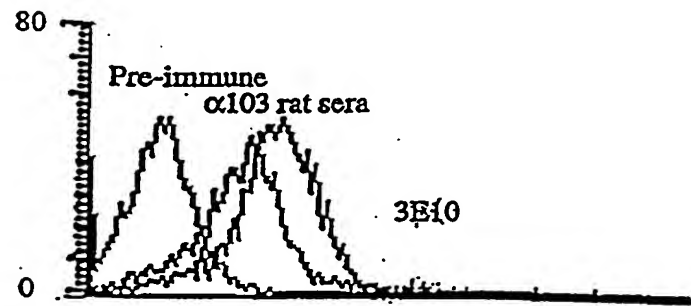
AE7



Dorris



D10.G4



DAX

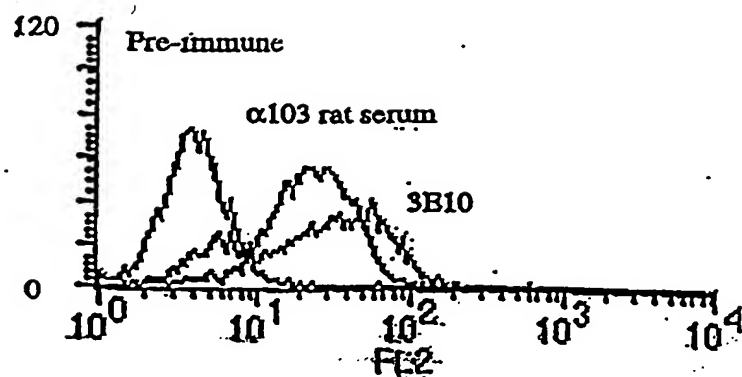


FIGURE 25

10004633-120401

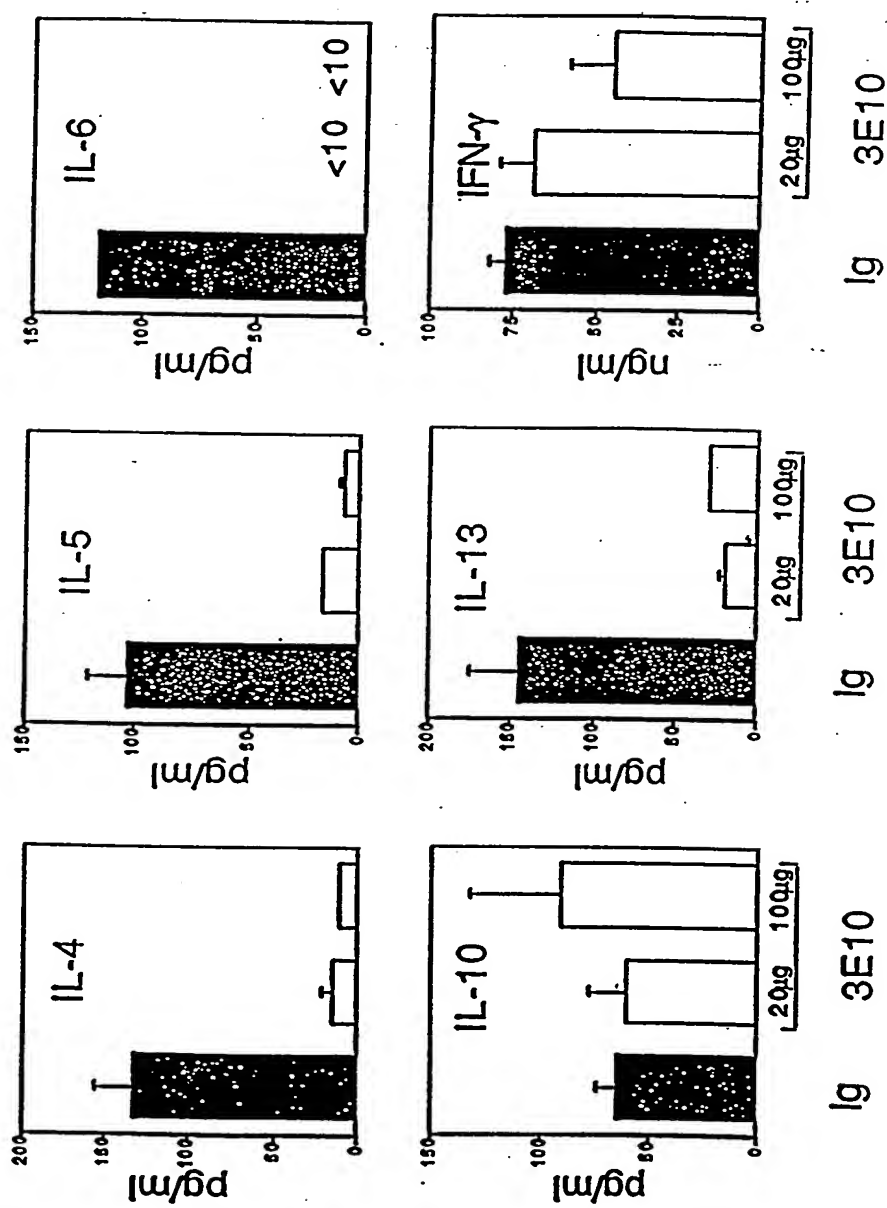


FIGURE 26

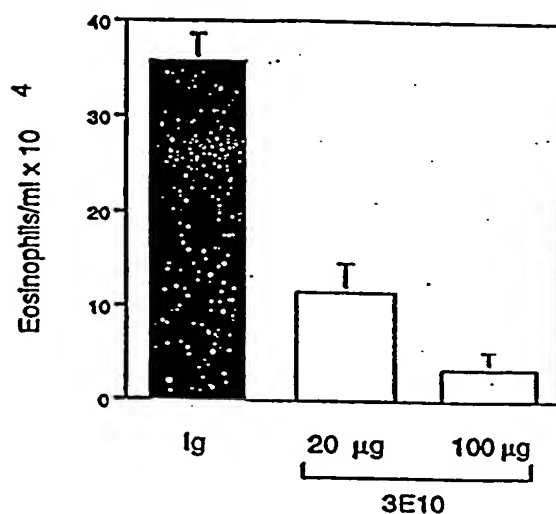


FIGURE 27A

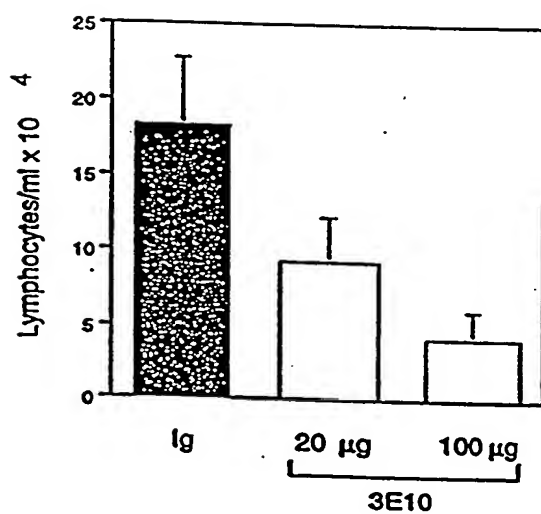


FIGURE 27B

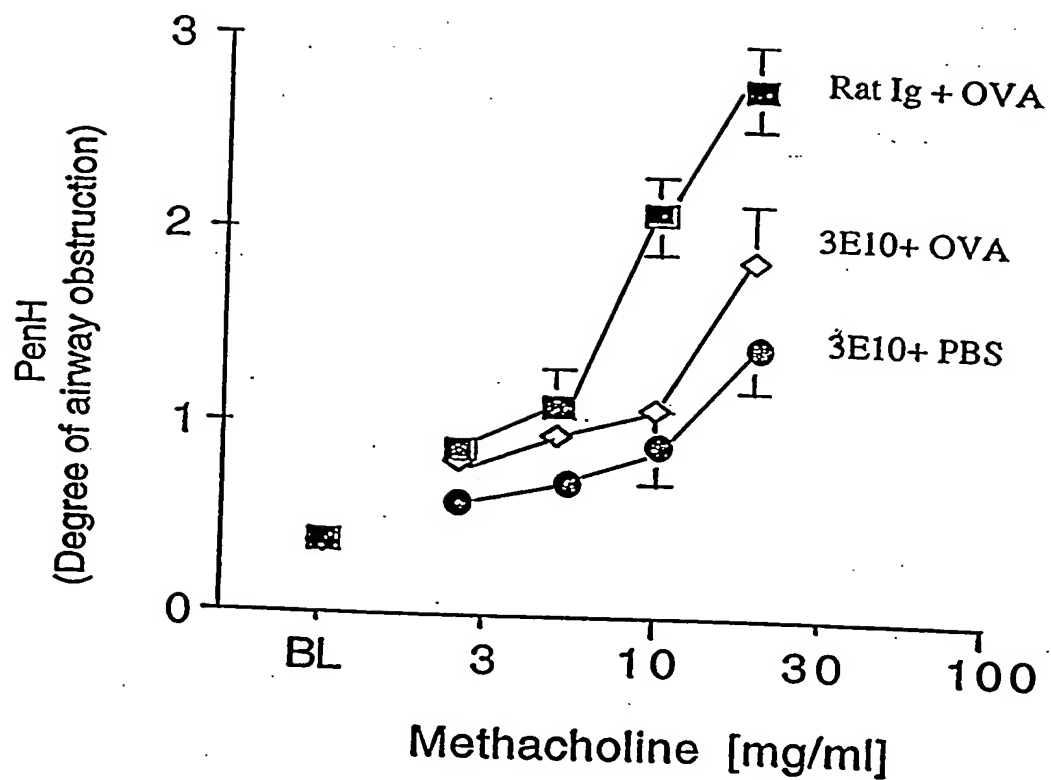


FIGURE 28

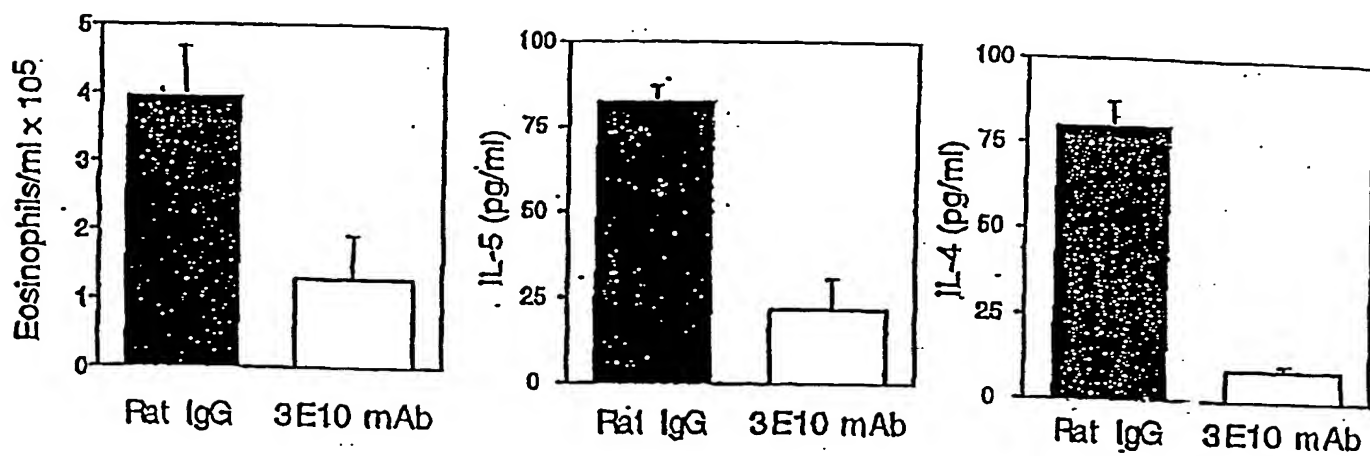


FIGURE 29A

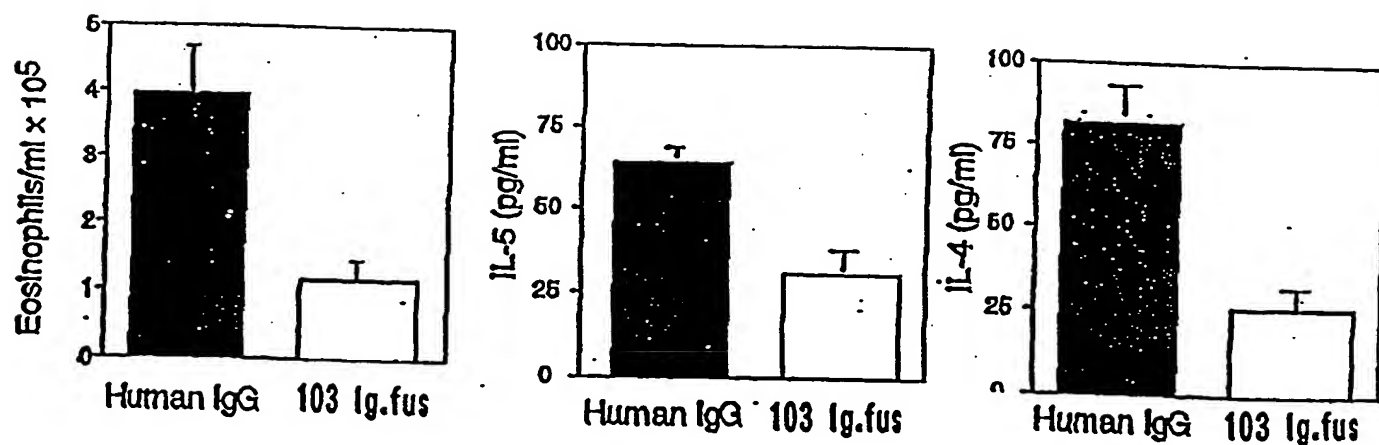


FIGURE 29B

T0402T"EE94000T

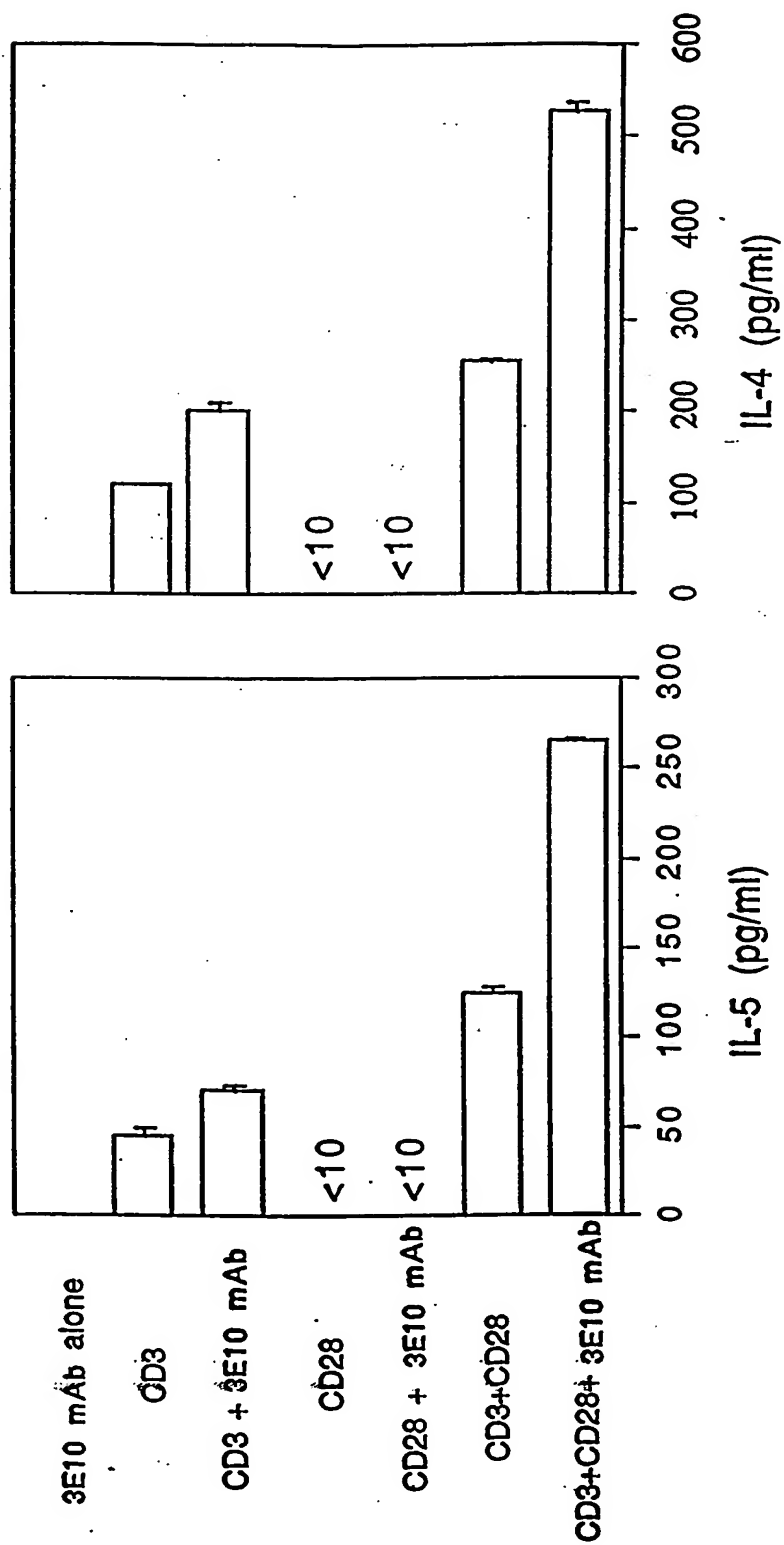


FIG. 30

Renal histology at 72hrs post
reperfusion

+RbIg

+a200

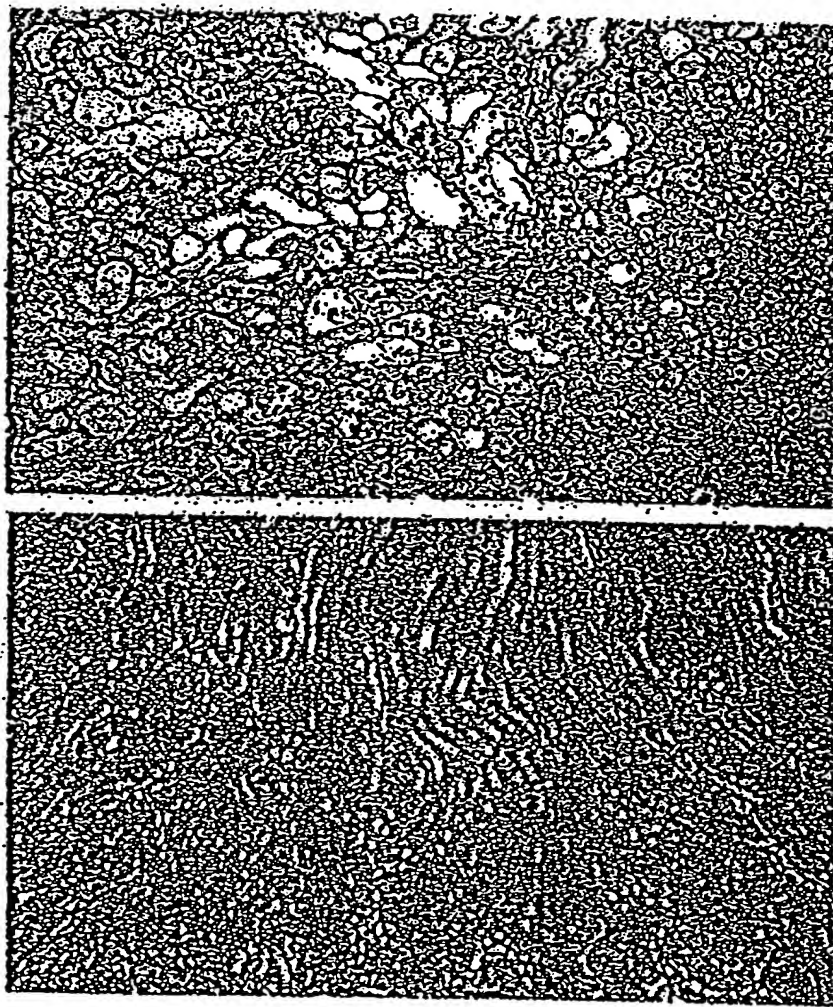


FIG. 31

Blockage of gene 200 during renal ischemia/reperfusion injury

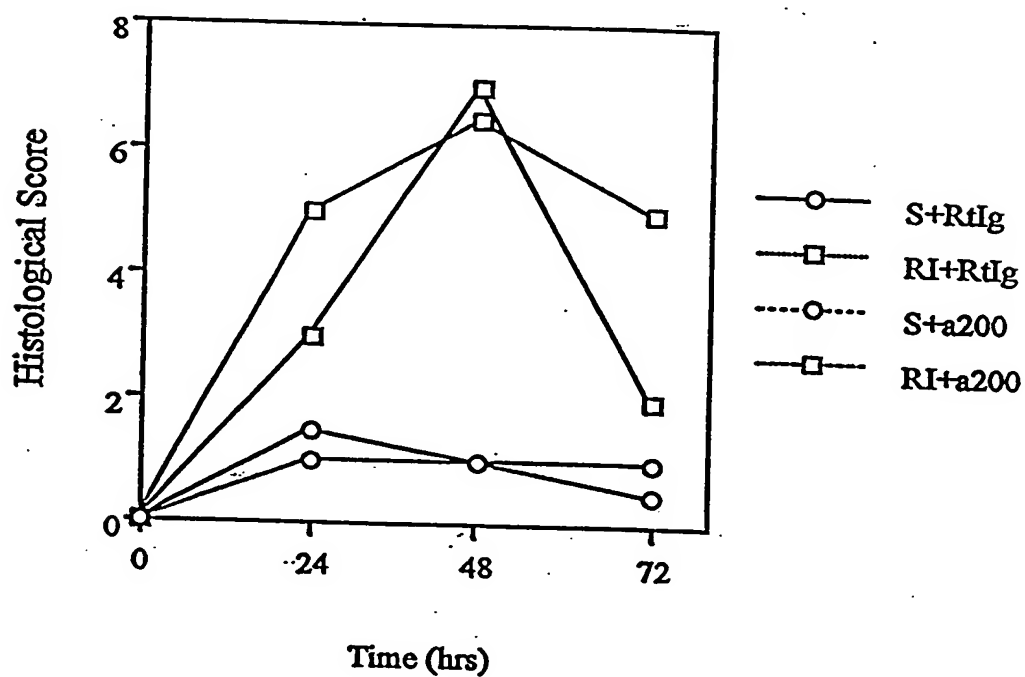


FIG. 32